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(54) Title: CRYSTAL STRUCTURE OF ENZYME AND USES THEREOF

(57) Abstract: The invention provides crystalline forms of a polypeptide corresponding to the catalytic domain of Aurora kinase. The active site ATP binding pocket is defined by its amino acid residues and their atomic coordinates. This structure may be used to select or design chemical modulators of Aurora kinase, particularly Aurora inhibitors. These modulators may be used to treat diseases of cell proliferation, e.g. cancer.

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CRYSTAL STRUCTURE OF ENZYME AND USES THEREOF

Field of the Invention

This invention relates to crystallised Aurora A kinase and the use of its three-dimensional structure to investigate Aurora kinase homologues and to design Aurora kinase modulators.

Background of the Invention

Proteins such as enzymes involved in physiological and pathological processes are important targets in the development of pharmaceutical compounds and treatments. Knowledge of the three dimensional (tertiary) structure of proteins allows the rational design of mimics or modulators of such proteins. By searching structural databases using structural parameters derived from the protein of interest, it is possible to select molecular structures that may mimic or interact with these parameters. It is then possible to synthesise the selected molecular structure and test its activity. Alternatively, the structural parameters derived from the protein of interest may be used to design and synthesise a mimic or modulator with the desired activity. Such mimics or modulators may be useful as therapeutic agents for treating certain diseases. For example, WO98/07835 discloses crystal structures of a protein tyrosine kinase optionally complexed with one or more compounds. The atomic coordinates of the enzyme structures and any of the bound compounds are used to determine the three-dimensional structures of kinases with unknown structure and to identify modulators of kinase functions. As another example, WO99/01476 discloses the crystal structures of anti-Factor IX Fab fragments (antibodies) and their use to identify and design new anticoagulant agents.

Knowledge of the three-dimensional structure of a protein is essential for the rational design of mimics or modulators of that protein. Lack of structural knowledge is a barrier to the development of new mimics or modulators that may have extremely useful pharmaceutical properties.

In Eukaryotes, the cell cycle is largely controlled by an ordered cascade of protein phosphorylation. Several families of protein kinases that play critical roles in this cascade have now been identified. The activity of many of these kinases is increased in human tumours when compared to normal tissue. This can occur by either increased levels of expression of the protein (as a result of gene amplification for example), or by changes in expression of co-activators or inhibitory proteins.

The first identified, and most widely studied of these cell cycle regulators have been the cyclin-dependent kinases (or CDKs). Activity of specific CDKs at specific times is essential for both initiation and coordinated progress through the cell cycle. For example, the CDK4 protein appears to control entry into the cell cycle (the G0-G1-S transition) by phosphorylating the retinoblastoma gene product pRb. This stimulates the release of the transcription factor E2F from pRb, which then acts to increase the transcription of genes necessary for entry into S phase. The catalytic activity of CDK4 is stimulated by binding to a partner protein, Cyclin D1. One of the first demonstrations of a direct link between cancer and the cell cycle was made with the observation that the Cyclin D1 gene was amplified and cyclin D1 protein levels increased (and hence the activity of CDK4 increased) in many human tumours (Reviewed in Sherr, 1996, Science 274: 1672-1677; Pines, 1995, Seminars in Cancer Biology 6: 63-72). Other studies have shown that negative regulators of CDK function are frequently down-regulated or deleted in human tumours, again leading to inappropriate activation of these kinases (Loda et al., 1997, Nature Medicine 3(2): 231-234; Gemma et al., 1996, International Journal of Cancer 68(5): 605-11; Elledge et al. 1996, Trends in Cell Biology 6; 388-392).

More recently, protein kinases that are structurally distinct from the CDK family have been identified which play critical roles in regulating the cell cycle and which also appear to be important in oncogenesis. These include the newly-identified human homologues of the *Drosophila* Aurora and *S. cerevisiae* Ipl1 proteins. *Drosophila* Aurora and *S. cerevisiae* Ipl1, which are highly homologous at the amino acid sequence level, encode serine/threonine protein kinases. Both Aurora and Ipl1 are known to be involved in controlling the transition from the G2 phase of the cell cycle through mitosis, centrosome function, formation of a mitotic spindle and proper chromosome separation / segregation into daughter cells. The three human homologues of these genes, termed Aurora A, B and C, encode cell cycle regulated protein kinases. These show a peak of expression and kinase activity at the G2/M boundary (Aurora A, C) and in mitosis and cytokinesis (Aurora B). Several observations implicate the involvement of human Aurora proteins, in particular Aurora A in cancer. The Aurora A gene maps to chromosome 20q13, a region that is frequently amplified in human tumours including both breast and colon tumours. Aurora A may be the major target gene of this amplicon, since Aurora A DNA is amplified and Aurora A mRNA over expressed in greater than 50% of primary human colorectal cancers. In these tumours Aurora A protein levels appear greatly elevated compared to adjacent normal tissue. In addition, transfection of rodent fibroblasts

with human Aurora A leads to transformation, conferring the ability to grow in soft agar and form tumours in nude mice (Bischoff et al., 1998, The EMBO Journal. 117(11): 3052-3065). Other work has shown that artificial over expression of Aurora A leads to an increase in centrosome number and an increase in aneuploidy (Zhou et al., 1998, Nature Genetics. 20(2): 189-93).

Importantly, it has also been demonstrated that abrogation of Aurora A expression and function by antisense oligonucleotide treatment of human tumour cell lines (Bischoff and Ploughman, 1999, Trends in Cell Biology, 9(11): 454-459 or by a small molecule inhibitor of Aurora A kinase activity (Keen et al. 2001, poster #2455, American Association for Cancer Research annual meeting, New Orleans USA) leads to defects in mitosis, cell cycle arrest and exerts an antiproliferative effect in these tumour cell lines. This indicates that inhibition of the function of Aurora A will have an antiproliferative effect that may be useful in the treatment of human tumours and other hyperproliferative diseases.

In order to design inhibitors of Aurora A kinase, it is necessary to know the three-dimensional structure of Aurora A kinase, in complex with various lead compounds. To date, the three-dimensional structure of Aurora A kinase has not been available. Further, it has not been possible to obtain crystals of any part of Aurora of sufficient quality to allow determination of the structure of the kinase domain including the site of inhibition.

Summary of the Invention

The present invention relates to the previously unknown three-dimensional structure of human Aurora A kinase. As described herein, the Applicants have overcome the difficulties encountered by others and have produced crystals of the Aurora A kinase catalytic domain that are of sufficient quality to determine the three-dimensional structure of the protein by X-ray diffraction methods. In addition, the Applicants have determined the three-dimensional crystal structure of the kinase catalytic domain of Aurora A kinase in a complex with the ATP analogue AMP-PNP, as well as the three-dimensional crystal structure of the Aurora A kinase catalytic domain in complex with a synthetic inhibitor. There is a clear need for this structural information to enable identification and structure-based design of new Aurora kinase modulators (particularly inhibitors) for the treatment of various diseases or conditions and in particular diseases of cell proliferation such as cancer. The methods described herein allow the determination of the three-dimensional structures of Aurora A kinase, as well as other Aurora

kinases, in complex with numerous inhibitors of interest to aid in the rational design of modulators that will treat diseases of cell proliferation.

Brief Description of the Drawings

Figure 1 is a schematic representation of the structure of the [T287D] Aurora A complex with AMP-PNP. The inhibitor has 2 conformations.

Figure 2a is a schematic representation of the structure of Aurora A in complex with a synthetic inhibitor drawn in approximately the same orientation as Figure 1.

Figure 2b is a schematic representation of Aurora A in complex with a synthetic inhibitor, rotated so as to show the extended inhibitor occupying a long active site binding pocket.

Figure 3 is a graph of the activity of [T287D]Aurora A as a function of pH.

Detailed Description of the Invention

This invention relates to crystals of Aurora A kinase and the use of the three-dimensional structure to investigate Aurora kinase homologues and to design Aurora kinase modulators (preferably inhibitors). It further relates to crystals of Aurora kinase, particularly Aurora A kinase, or the catalytic portion thereof, complexed or uncomplexed as described, of sufficient quality to determine the three dimensional (tertiary) structure of the polypeptide by X-ray diffraction methods.

According to a first aspect of the invention, the Applicants provide two crystalline forms of a polypeptide comprising the catalytic domain of Aurora A kinase. One crystalline form is obtained when we crystallise [T287D]Aurora A(122-396) in the presence of the ATP-analogue AMP-PNP. The second crystalline form is obtained when we crystallise GSHM-[T287D]Aurora A(122-400) in the presence of a synthetic inhibitor. (Amino acid residues in Aurora A are numbered by taking the first amino acid immediately after the initial methionine as amino acid number one). In one embodiment, the first crystalline form has the space group $P3_221$. In another embodiment, the first crystalline form has the unit cell dimensions $a = b = 86.55$, $c = 78.34$ Å, $\alpha = \beta = 90$ and $\gamma = 120°$. In another embodiment, the second crystalline form has space group $P2_1$. In another embodiment, the second crystalline form has the unit

cell dimensions a = 52.6, b = 88.4, c = 67.8 Å, $\alpha = \gamma = 90$ and $\beta = 90.01°$. In another embodiment, these crystalline forms are described by three-dimensional sets of x,y,z-coordinates (Tables 1 and 2) for each atom in the complex representing the unique repeating motif in the crystal. Table 1 contains the coordinates for the complex molecule in the first crystalline form; Table 2 contains the coordinates for two independent complex molecules in the asymmetric unit (smallest unique repeating unit) in the second crystalline form. In another embodiment, these crystalline forms contain a numerical definition of a binding site, approximated by the set of all residues within a 5 Å contact distance from any atom in either inhibitor. The binding site is defined by the x,y,z-coordinates of atoms in the set of amino acid residues (set A) given by the list Arg136, Leu138, Gly139, Lys140, Gly141, Val146, Ala 159, Lys161, Leu163, Val177, Glu180, Val181, Ile183, Gln184, Leu193, Leu195, Leu207, Leu209, Glu210, Tyr211, Ala212, Pro213, Leu214, Gly215, Thr216, Arg219, Glu259, Asn260, Leu262, Ala272, Asp273, Phe274, Gly275, Trp276, Ser277, Val278, and His279, the atomic coordinates being listed in Tables 1 and 2. The binding site is may be defined in any alternate crystalline form, homologue, variant or mutant wherein the binding site has a root mean square deviation from all atoms of the amino acid residues of not more than 1.0 Å from a least-flexible subset (set B) of the binding site that includes the amino acid residues Arg136, Leu138, Gly139, Val146, Ala159, Lys161, Leu163, Ile183, Gln184, Leu193, Leu195, Leu207, Leu209, Glu210, Tyr211, Ala212, Pro213, Leu214, Gly215, Thr216, Arg219, Glu259, Asn260 and Leu262, each having coordinates as described in Tables 1 and 2.

In another embodiment, the first crystalline form comprises a binding site defined by amino acid residues Leu138, Gly139, Val146, Lys161, Val177, Arg178, Arg179, Glu180, Val181, Glu182, Ile183, Gln184, Leu193, Leu209, Tyr211, Ala212, Gly215, Thr216, Glu259, Asn260, Leu262, Ala272, Asp273, Phe274, Gly275, Trp276, Ser277, Val278 and His 279, each having the coordinated listed in Table 1a. An alternative crystalline form, homologue, variant or mutant wherein the binding site has a root mean square deviation from the backbone atoms of the amino acid residues of not more than 1.5 Å, and preferably not more than 1.0 Å is also provided.

In another embodiment, the crystalline forms additionally comprise Aurora kinase inhibitors in complex with the catalytic domain of Aurora kinase including any of the above embodiments of the crystalline form.

Another aspect of the invention relates to a method of designing an Aurora chemical modulator using the atomic coordinates of a crystalline form according to any of the above embodiments.

Another aspect of the invention relates to a method of selecting an Aurora chemical modulator using the atomic coordinates of a crystalline form according to any of the above embodiments.

Another aspect of the invention relates to a method of designing or selecting an Aurora chemical modulator using the atomic coordinates of any other protein, e.g. PKA, which has been shown by this invention to have structural similarity to Aurora.

Another aspect of the invention relates to a method of designing an Aurora protein using the atomic coordinates of a crystalline form according to any of the above embodiments.

Another aspect of the invention relates to a method of designing or selecting an Aurora modulator comprising the steps of:

exploring the atomic coordinates of Aurora (Tables 1 and 2) for information on the three-dimensional characteristics of the protein surface;

arriving at an alternative overlapping or non-overlapping binding pocket to the active site ATP binding pocket; and

selecting or designing an Aurora modulator using the binding pocket information.

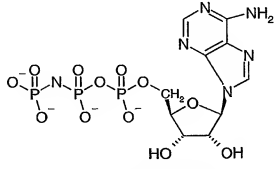
Another aspect of the invention relates to a method of determining the three-dimensional structure of a crystal form of Aurora kinase, referred to as a second or new crystal or crystal form of Aurora kinase, comprising the step of applying difference Fourier or molecular replacement methods using the atomic coordinates of an original crystal of Aurora kinase (from Table 1 or 2) to model the structure of a new crystal, wherein the active site ATP binding pocket of the new crystal is equivalent to that in the first crystal. In a specific embodiment, the invention is a method of determining the three-dimensional structure of a crystal form of Aurora kinase A comprising the step of applying difference Fourier or molecular replacement methods using the atomic coordinates of an original (first) crystal of Aurora kinases (from Table 1 or 2) to model the structure of a new crystal or new crystal form of Aurora kinase A, wherein the active site ATP binding pocket of the new crystal is equivalent to that in the original (first) crystal.

In particular provided herein are crystalline forms of a polypeptide including the catalytic domain of an Aurora A protein. The catalytic domain may be found within the complete protein or within a fragment of the protein. The catalytic domain may be also

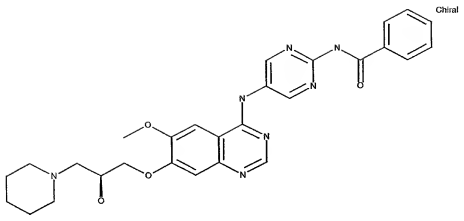
derived from a wild-type Aurora A enzyme or from an Aurora A mutant, homologue or variant. A mutant is a wild type Aurora A protein having one or more changes in its amino acid sequence. An Aurora mutant may have the same activity as the wild type protein, may have modified activity or may be inactive. A variant is a wild type or mutant protein having one or more portions of its sequence removed, or an additional sequence or sequences added, so that the variant is a different length from the wild type or mutant protein. A variant usually has the same activity as the original wild type or mutant protein. A homologue is a related protein in which some parts of the amino acid sequence are the same as in the original protein. Aurora B and Aurora C, for example, are homologues of Aurora A.

The invention relates to crystals of sufficient quality to determine the three dimensional structure to high resolution of any portion, mutant, variant or homologue of Aurora A involving the catalytic domain.

According to a further aspect of the invention, we provide crystalline forms of a polypeptide containing the Aurora A catalytic domain in complex with small molecular weight inhibitor molecules. For example, the inhibitor molecule might be a non-hydrolysable analogue of ATP. Such analogues include, for example, formula I (AMP-PNP). As another example, the inhibitor might be a molecule synthesised chemically. Such molecules include, for example, formula II.



Formula I: AMP-PNP



Formula II

Another aspect of the invention is the unique shape of the active site ATP binding pocket in Aurora. Using X-ray crystallography, we have determined the three-dimensional molecular structure of an Aurora A catalytic domain. Resulting from this, we have determined the unique shape of an Aurora A active site ATP binding pocket (defined by the atomic coordinates of its constituent amino acids). Furthermore, we have determined the spatial arrangement of an Aurora A substrate analogue and an inhibitor molecule relative to the Aurora A active site binding pocket. This structural information can be stored on a computer-readable medium and may be used for rational drug design.

One of the difficulties in studying kinases in general is obtaining active protein. In order to be activated, certain kinases need to be phosphorylated at one or more key amino acid residues. It may be experimentally difficult to obtain 100% pure phosphorylated protein. Different phosphorylation states may have different conformations. Those in the art realise that such heterogeneities in the protein sample can severely impede the ability to form large well-ordered crystals. In Aurora A, phosphorylation of Thr 287 is necessary for activation of the kinase. Replacement of Thr-287 by Asp (an Aurora A mutant called [T287D] Aurora A) provides a mimic of the active protein which can be provided as a homogeneous sample. The [T287D]Aurora A mutant is constitutively active. Thus, preparation of this mutant conveniently addresses both issues of activity and crystallisability.

One of the major hurdles in the crystallisation of multidomain proteins is their flexibility. To increase the chances of crystallising Aurora A, an enzyme construct limited to the catalytic domain was used. This provided a more rigid and compact domain. Catalytic domain constructs can be designed by comparing the amino acid sequence to other kinases of known structure, and defining start and end residues for the polypeptide encompassing the

Aurora A catalytic domain by analogy. This gives numerous possible construct variants, which include the catalytic domain. In order to increase further the chances of crystallising Aurora A, experimental evidence was sought as to which catalytic domain construct would be the most compact while retaining integrity as a folding unit. Limited proteolysis was carried out using endoproteinase Glu-C from Staphylococcus aureus V8 on the catalytic domain. This defined the catalytic domain boundaries to be within residues 122 to 396. Other similar constructs may be obtained through similar procedures, using, for example, different proteases for the limited proteolysis experiment. Such a procedure is exemplified by our preparation, crystallisation and determination of the structure of two Aurora A catalytic domain polypeptides. The structure of [T287D]Aurora A(122-396) in complex with the non-hydrolysable ATP analogue AMP-PNP is shown in Fig. 1. The structure of GSHM-[T287D]Aurora A(122-400) in complex with the synthetic Aurora inhibitor of formula II is shown in Fig. 2a and 2b.

The AMP-PNP molecule occupies a cleft between the N-terminal domain (residues 125 to 208) and the C-terminal domain (residues 215 to 374). Comparison with other kinases demonstrates that this cleft represents a portion of the ATP binding site. Therefore, we have identified the active site ATP binding pocket of Aurora. The electron density shows evidence for the AMP-PNP adopting a dual conformation. In both conformations, the adenine ring and ribose moiety occupy similar pockets with the adenine nitrogen atoms N1 and N6 making classical interactions with main chain atoms in the hinge region (residues 209 to 214) of the enzyme. N1 forms a hydrogen bond with the main chain nitrogen of Ala-212 while N6 forms a hydrogen bond to the peptide carbonyl group of Glu-210. However, torsion angle differences elsewhere in the molecule allow the alpha and beta phosphate groups to occupy alternative pockets. No electron density is apparent in either conformation for the gamma phosphate group of the AMP-PNP molecule. In conformation 1, the beta phosphate group makes polar interactions with the O oxygen atoms of Ser 277 and the side-chain of Asn260, while in conformation 2, the beta phosphate makes polar interactions with the amide carbonyl of –Glu-259 and with a water molecule (Wat-542 in this structure).

From the three-dimensional structure that we have determined for [T287D] Aurora A, we establish that the AMP-PNP binding pocket, which is the active site ATP binding pocket, is uniquely defined by the atomic co-ordinates of its constituent amino acid residues, the coordinates being listed in Tables 1 and 2. An equivalent ATP binding pocket may also be defined having the same co-ordinates as detailed in Table 1 and with the same constitutent

amino acid residues except that Lys140 and Gly141 in Table 1 and replaced with Ala140 and Ala141, whereby such a table is referred to hereonin as Table 1a.

Table 1: coordinates of [T287D] Aurora A (122-396) in complex with AMP-PNP

```
REMARK coordinates from restrained individual B-factor refinement
REMARK refinement resolution: 500 - 2.2 A
REMARK starting r= 0.2325 free_r= 0.2841
REMARK final    r= 0.2317 free_r= 0.2832
REMARK B rmsd for bonded mainchain atoms=  1.663  target= 1.5
REMARK B rmsd for bonded sidechain atoms=  2.408  target= 2.0
REMARK B rmsd for angle mainchain atoms=  2.759  target= 2.0
REMARK B rmsd for angle sidechain atoms=  3.575  target= 2.5
REMARK wa= 2.95383
REMARK rweight=9.122374E-02
REMARK target= mlf  steps= 40
REMARK sg=P3(2)21 a=86.551 b=86.551 c=78.337 alpha=90 beta=90 gamma=120
REMARK parameter file 1  : MSI_CNX_TOPPAR:protein_rep.param
REMARK parameter file 2  : anp.par
REMARK parameter file 3  : fra.par
REMARK parameter file 4  : MSI_CNX_TOPPAR:water_rep.param
REMARK parameter file 5  : gly.par
REMARK molecular structure file: generate.mtf
REMARK input coordinates: minimize.pdb
REMARK reflection file= aurora-dl.cv
REMARK ncs= none
REMARK B-correction resolution: 6.0 - 2.2
REMARK initial B-factor correction applied to fobs :
REMARK    B11=  -2.797 B22=  -2.797 B33=   5.593
REMARK    B12=  -2.312 B13=   0.000 B23=   0.000
REMARK B-factor correction applied to coordinate array B:    0.127
REMARK bulk solvent:(Mask)density level=0.392672e/A^3,B-factor=81.6283 A^2
REMARK reflections with |Fobs|/sigma_F < 0.0 rejected
REMARK reflections with |Fobs| > 1000 * rms(Fobs) rejected
REMARK theoretical total number of refl. in resol. range: 17604 (100.0%)
REMARK number of unobserved reflections (no entry or |F|=0): 841 (4.8%)
REMARK number of reflections rejected:                  0 (   0.0 % )
REMARK total number of reflections used:            16763 (  95.2 % )
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REMARK number of reflections in test set:             821 (   4.7 % )
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ATOM      3  O   ALA A 125     45.008  59.073  14.092  1.00 81.57   A    O
ATOM      4  N   ALA A 125     43.336  60.097  11.271  1.00 79.55   A    N
ATOM      5  CA  ALA A 125     44.170  59.002  11.840  1.00 80.04   A    C
ATOM      6  N   GLN A 126     42.809  58.655  13.835  1.00 79.21   A    N
ATOM      7  CA  GLN A 126     42.542  58.531  15.272  1.00 77.20   A    C
ATOM      8  CB  GLN A 126     41.980  59.849  15.817  1.00 78.38   A    C
ATOM      9  CG  GLN A 126     42.496  60.222  17.206  1.00 78.91   A    C
ATOM     10  CD  GLN A 126     41.965  59.321  18.304  1.00 79.23   A    C
ATOM     11  OE1 GLN A 126     42.092  58.098  18.238  1.00 80.18   A    O
ATOM     12  NE2 GLN A 126     41.372  59.925  19.328  1.00 78.24   A    N
ATOM     13  C   GLN A 126     41.550  57.382  15.510  1.00 74.64   A    C
ATOM     14  O   GLN A 126     41.834  56.234  15.151  1.00 74.20   A    O
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ATOM     27  C   TRP A 127     39.067  56.021  15.004  1.00 61.91   A    C
ATOM     28  O   TRP A 127     39.034  56.724  14.001  1.00 62.11   A    O
ATOM     29  N   ALA A 128     38.836  54.712  14.975  1.00 57.60   A    N
ATOM     30  CA  ALA A 128     38.491  54.016  13.740  1.00 52.69   A    C
```

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ATOM	33	O	ALA	A	128	37.565	52.372	15.220	1.00	48.81	A	O
ATOM	34	N	LEU	A	129	36.875	52.308	13.082	1.00	47.90	A	N
ATOM	35	CA	LEU	A	129	35.975	51.176	13.293	1.00	47.52	A	C
ATOM	36	CB	LEU	A	129	35.235	50.836	11.991	1.00	46.25	A	C
ATOM	37	CG	LEU	A	129	34.125	49.775	12.047	1.00	47.39	A	C
ATOM	38	CD1	LEU	A	129	33.068	50.164	13.079	1.00	45.16	A	C
ATOM	39	CD2	LEU	A	129	33.488	49.630	10.671	1.00	48.56	A	C
ATOM	40	C	LEU	A	129	36.706	49.936	13.815	1.00	48.62	A	C
ATOM	41	O	LEU	A	129	36.170	49.199	14.645	1.00	46.32	A	O
ATOM	42	N	ALA	A	130	37.930	49.724	13.333	1.00	49.46	A	N
ATOM	43	CA	ALA	A	130	38.750	48.584	13.742	1.00	50.75	A	C
ATOM	44	CB	ALA	A	130	40.037	48.538	12.907	1.00	50.42	A	C
ATOM	45	C	ALA	A	130	39.098	48.610	15.233	1.00	51.11	A	C
ATOM	46	O	ALA	A	130	39.559	47.611	15.782	1.00	51.23	A	O
ATOM	47	N	ASP	A	131	38.896	49.752	15.883	1.00	51.02	A	N
ATOM	48	CA	ASP	A	131	39.183	49.863	17.310	1.00	51.74	A	C
ATOM	49	CB	ASP	A	131	39.353	51.328	17.735	1.00	55.51	A	C
ATOM	50	CG	ASP	A	131	40.539	52.012	17.080	1.00	57.37	A	C
ATOM	51	OD1	ASP	A	131	40.515	52.230	15.852	1.00	60.16	A	O
ATOM	52	OD2	ASP	A	131	41.496	52.344	17.804	1.00	60.43	A	O
ATOM	53	C	ASP	A	131	38.041	49.282	18.134	1.00	50.19	A	C
ATOM	54	O	ASP	A	131	38.147	49.195	19.352	1.00	51.36	A	O
ATOM	55	N	PHE	A	132	36.956	48.881	17.474	1.00	48.84	A	N
ATOM	56	CA	PHE	A	132	35.779	48.370	18.181	1.00	47.79	A	C
ATOM	57	CB	PHE	A	132	34.600	49.327	17.969	1.00	47.00	A	C
ATOM	58	CG	PHE	A	132	34.877	50.743	18.370	1.00	45.30	A	C
ATOM	59	CD1	PHE	A	132	34.853	51.119	19.711	1.00	45.44	A	C
ATOM	60	CD2	PHE	A	132	35.148	51.708	17.404	1.00	43.30	A	C
ATOM	61	CE1	PHE	A	132	35.093	52.443	20.087	1.00	41.66	A	C
ATOM	62	CE2	PHE	A	132	35.390	53.034	17.772	1.00	43.84	A	C
ATOM	63	CZ	PHE	A	132	35.361	53.399	19.115	1.00	42.35	A	C
ATOM	64	C	PHE	A	132	35.278	46.982	17.801	1.00	48.37	A	C
ATOM	65	O	PHE	A	132	35.501	46.505	16.689	1.00	49.60	A	O
ATOM	66	N	GLU	A	133	34.575	46.350	18.740	1.00	47.46	A	N
ATOM	67	CA	GLU	A	133	33.951	45.053	18.501	1.00	45.33	A	C
ATOM	68	CB	GLU	A	133	34.214	44.082	19.661	1.00	48.04	A	C
ATOM	69	CG	GLU	A	133	34.835	42.759	19.214	1.00	49.09	A	C
ATOM	70	CD	GLU	A	133	34.935	41.725	20.325	1.00	49.60	A	C
ATOM	71	OE1	GLU	A	133	33.892	41.172	20.745	1.00	49.55	A	O
ATOM	72	OE2	GLU	A	133	36.064	41.464	20.778	1.00	49.86	A	O
ATOM	73	C	GLU	A	133	32.460	45.384	18.418	1.00	44.56	A	C
ATOM	74	O	GLU	A	133	31.932	46.080	19.282	1.00	41.15	A	O
ATOM	75	N	ILE	A	134	31.785	44.899	17.380	1.00	44.52	A	N
ATOM	76	CA	ILE	A	134	30.364	45.180	17.194	1.00	44.87	A	C
ATOM	77	CB	ILE	A	134	30.033	45.362	15.700	1.00	43.36	A	C
ATOM	78	CG2	ILE	A	134	28.567	45.739	15.540	1.00	44.27	A	C
ATOM	79	CG1	ILE	A	134	30.968	46.409	15.080	1.00	45.76	A	C
ATOM	80	CD1	ILE	A	134	30.975	47.777	15.776	1.00	43.59	A	C
ATOM	81	C	ILE	A	134	29.420	44.119	17.759	1.00	45.96	A	C
ATOM	82	O	ILE	A	134	29.603	42.927	17.514	1.00	46.32	A	O
ATOM	83	N	GLY	A	135	28.396	44.571	18.487	1.00	44.99	A	N
ATOM	84	CA	GLY	A	135	27.425	43.661	19.083	1.00	45.95	A	C
ATOM	85	C	GLY	A	135	26.050	43.706	18.438	1.00	44.79	A	C
ATOM	86	O	GLY	A	135	25.918	44.096	17.281	1.00	45.37	A	O
ATOM	87	N	ARG	A	136	25.014	43.330	19.183	1.00	46.84	A	N
ATOM	88	CA	ARG	A	136	23.652	43.314	18.630	1.00	47.11	A	C
ATOM	89	CB	ARG	A	136	22.665	42.699	19.629	1.00	47.09	A	C
ATOM	90	CG	ARG	A	136	22.462	43.505	20.909	1.00	45.16	A	C
ATOM	91	CD	ARG	A	136	21.296	42.979	21.736	1.00	41.59	A	C
ATOM	92	NE	ARG	A	136	21.296	43.550	23.080	1.00	41.35	A	N
ATOM	93	CZ	ARG	A	136	20.457	44.490	23.507	1.00	41.75	A	C
ATOM	94	NH1	ARG	A	136	19.527	44.978	22.701	1.00	41.10	A	N
ATOM	95	NH2	ARG	A	136	20.553	44.949	24.745	1.00	41.12	A	N
ATOM	96	C	ARG	A	136	23.116	44.680	18.205	1.00	47.41	A	C
ATOM	97	O	ARG	A	136	23.482	45.710	18.770	1.00	46.21	A	O
ATOM	98	N	PRO	A	137	22.231	44.696	17.197	1.00	49.15	A	N
ATOM	99	CD	PRO	A	137	21.994	43.557	16.295	1.00	50.53	A	C
ATOM	100	CA	PRO	A	137	21.607	45.910	16.659	1.00	50.22	A	C
ATOM	101	CB	PRO	A	137	20.948	45.420	15.373	1.00	49.86	A	C
ATOM	102	CG	PRO	A	137	21.781	44.245	14.978	1.00	49.74	A	C

ATOM	103	C	PRO	A	137	20.580	46.507	17.620	1.00	51.56	A	C
ATOM	104	O	PRO	A	137	19.619	45.841	18.007	1.00	52.67	A	O
ATOM	105	N	LEU	A	138	20.783	47.760	18.005	1.00	51.44	A	N
ATOM	106	CA	LEU	A	138	19.851	48.430	18.908	1.00	52.81	A	C
ATOM	107	CB	LEU	A	138	20.589	49.498	19.721	1.00	52.13	A	C
ATOM	108	CG	LEU	A	138	21.156	49.087	21.086	1.00	51.35	A	C
ATOM	109	CD1	LEU	A	138	21.737	47.694	21.033	1.00	54.20	A	C
ATOM	110	CD2	LEU	A	138	22.201	50.093	21.516	1.00	50.21	A	C
ATOM	111	C	LEU	A	138	18.710	49.064	18.114	1.00	53.48	A	C
ATOM	112	O	LEU	A	138	17.604	49.235	18.620	1.00	53.15	A	O
ATOM	113	N	GLY	A	139	18.990	49.401	16.860	1.00	55.10	A	N
ATOM	114	CA	GLY	A	139	17.992	50.015	16.009	1.00	55.12	A	C
ATOM	115	C	GLY	A	139	18.494	50.122	14.586	1.00	57.30	A	C
ATOM	116	O	GLY	A	139	19.684	50.365	14.348	1.00	55.60	A	O
ATOM	117	N	LYS	A	140	17.585	49.930	13.636	1.00	57.79	A	N
ATOM	118	CA	LYS	A	140	17.920	50.004	12.222	1.00	59.68	A	C
ATOM	119	CB	LYS	A	140	17.898	48.612	11.604	1.00	60.43	A	C
ATOM	120	C	LYS	A	140	16.902	50.897	11.534	1.00	61.09	A	C
ATOM	121	O	LYS	A	140	15.735	50.910	11.912	1.00	61.20	A	O
ATOM	122	N	GLY	A	141	17.337	51.648	10.530	1.00	62.18	A	N
ATOM	123	CA	GLY	A	141	16.413	52.525	9.834	1.00	62.70	A	C
ATOM	124	CB	GLY	A	141	15.841	53.534	10.803	1.00	65.14	A	C
ATOM	125	C	GLY	A	141	17.012	53.241	8.640	1.00	62.45	A	C
ATOM	126	O	GLY	A	141	18.188	53.082	8.325	1.00	61.72	A	O
ATOM	127	N	ALA	A	142	16.171	54.048	7.999	1.00	62.55	A	N
ATOM	128	CA	ALA	A	142	16.522	54.811	6.806	1.00	61.63	A	C
ATOM	129	CB	ALA	A	142	15.351	55.713	6.416	1.00	62.21	A	C
ATOM	130	C	ALA	A	142	17.793	55.641	6.903	1.00	60.80	A	C
ATOM	131	O	ALA	A	142	18.502	55.816	5.910	1.00	59.56	A	O
ATOM	132	N	PHE	A	143	18.088	56.152	8.091	1.00	59.81	A	N
ATOM	133	CA	PHE	A	143	19.266	56.986	8.255	1.00	58.87	A	C
ATOM	134	CB	PHE	A	143	18.913	58.170	9.153	1.00	61.93	A	C
ATOM	135	CG	PHE	A	143	18.150	59.246	8.439	1.00	64.91	A	C
ATOM	136	CD1	PHE	A	143	18.825	60.244	7.739	1.00	65.80	A	C
ATOM	137	CD2	PHE	A	143	16.759	59.225	8.407	1.00	65.92	A	C
ATOM	138	CE1	PHE	A	143	18.125	61.206	7.013	1.00	68.03	A	C
ATOM	139	CE2	PHE	A	143	16.048	60.182	7.683	1.00	67.18	A	C
ATOM	140	CZ	PHE	A	143	16.732	61.173	6.984	1.00	67.45	A	C
ATOM	141	C	PHE	A	143	20.514	56.275	8.755	1.00	56.62	A	C
ATOM	142	O	PHE	A	143	21.614	56.822	8.694	1.00	56.81	A	O
ATOM	143	N	GLY	A	144	20.343	55.050	9.235	1.00	54.51	A	N
ATOM	144	CA	GLY	A	144	21.472	54.289	9.728	1.00	51.51	A	C
ATOM	145	C	GLY	A	144	21.046	53.257	10.748	1.00	50.01	A	C
ATOM	146	O	GLY	A	144	19.864	52.914	10.849	1.00	50.62	A	O
ATOM	147	N	ASN	A	145	22.011	52.763	11.512	1.00	47.13	A	N
ATOM	148	CA	ASN	A	145	21.731	51.769	12.535	1.00	43.41	A	C
ATOM	149	CB	ASN	A	145	22.164	50.372	12.065	1.00	44.40	A	C
ATOM	150	CG	ASN	A	145	21.861	50.117	10.598	1.00	44.65	A	C
ATOM	151	OD1	ASN	A	145	22.761	50.118	9.761	1.00	46.61	A	O
ATOM	152	ND2	ASN	A	145	20.591	49.900	10.281	1.00	45.75	A	N
ATOM	153	C	ASN	A	145	22.517	52.127	13.788	1.00	40.16	A	C
ATOM	154	O	ASN	A	145	23.491	52.874	13.722	1.00	38.46	A	O
ATOM	155	N	VAL	A	146	22.082	51.599	14.927	1.00	36.92	A	N
ATOM	156	CA	VAL	A	146	22.780	51.818	16.188	1.00	35.73	A	C
ATOM	157	CB	VAL	A	146	21.908	52.590	17.221	1.00	35.98	A	C
ATOM	158	CG1	VAL	A	146	22.737	52.921	18.440	1.00	35.61	A	C
ATOM	159	CG2	VAL	A	146	21.353	53.868	16.610	1.00	38.31	A	C
ATOM	160	C	VAL	A	146	23.082	50.414	16.732	1.00	35.97	A	C
ATOM	161	O	VAL	A	146	22.224	49.537	16.688	1.00	35.59	A	O
ATOM	162	N	TYR	A	147	24.296	50.197	17.231	1.00	37.55	A	N
ATOM	163	CA	TYR	A	147	24.670	48.886	17.763	1.00	37.38	A	C
ATOM	164	CB	TYR	A	147	25.674	48.159	16.854	1.00	39.73	A	C
ATOM	165	CG	TYR	A	147	25.324	48.027	15.388	1.00	41.31	A	C
ATOM	166	CD1	TYR	A	147	25.614	49.052	14.484	1.00	43.72	A	C
ATOM	167	CE1	TYR	A	147	25.371	48.900	13.119	1.00	41.58	A	C
ATOM	168	CD2	TYR	A	147	24.773	46.847	14.890	1.00	42.29	A	C
ATOM	169	CE2	TYR	A	147	24.528	46.685	13.534	1.00	42.99	A	C
ATOM	170	CZ	TYR	A	147	24.832	47.712	12.656	1.00	43.10	A	C
ATOM	171	OH	TYR	A	147	24.619	47.533	11.312	1.00	43.57	A	O
ATOM	172	C	TYR	A	147	25.352	48.972	19.116	1.00	37.06	A	C
ATOM	173	O	TYR	A	147	25.950	49.985	19.466	1.00	36.75	A	O
ATOM	174	N	LEU	A	148	25.277	47.879	19.864	1.00	36.10	A	N

ATOM	175	CA	LEU	A	148	25.970	47.790	21.133	1.00	35.79	A C
ATOM	176	CB	LEU	A	148	25.466	46.574	21.911	1.00	38.69	A C
ATOM	177	CG	LEU	A	148	25.919	46.357	23.350	1.00	41.70	A C
ATOM	178	CD1	LEU	A	148	25.512	47.550	24.213	1.00	44.96	A C
ATOM	179	CD2	LEU	A	148	25.285	45.083	23.876	1.00	41.80	A C
ATOM	180	C	LEU	A	148	27.407	47.562	20.655	1.00	35.72	A C
ATOM	181	O	LEU	A	148	27.606	46.984	19.593	1.00	35.45	A O
ATOM	182	N	ALA	A	149	28.404	48.033	21.395	1.00	36.28	A N
ATOM	183	CA	ALA	A	149	29.791	47.829	20.989	1.00	37.35	A C
ATOM	184	CB	ALA	A	149	30.211	48.870	19.943	1.00	35.81	A C
ATOM	185	C	ALA	A	149	30.728	47.894	22.182	1.00	40.30	A C
ATOM	186	O	ALA	A	149	30.341	48.301	23.278	1.00	39.46	A O
ATOM	187	N	ARG	A	150	31.974	47.498	21.962	1.00	41.71	A N
ATOM	188	CA	ARG	A	150	32.956	47.506	23.026	1.00	45.19	A C
ATOM	189	CB	ARG	A	150	32.946	46.137	23.717	1.00	49.42	A C
ATOM	190	CG	ARG	A	150	33.892	45.984	24.888	1.00	52.01	A C
ATOM	191	CD	ARG	A	150	33.362	44.946	25.885	1.00	54.44	A C
ATOM	192	NE	ARG	A	150	32.854	43.742	25.231	1.00	55.30	A N
ATOM	193	CZ	ARG	A	150	32.082	42.837	25.828	1.00	53.68	A C
ATOM	194	NH1	ARG	A	150	31.729	42.996	27.095	1.00	54.04	A N
ATOM	195	NH2	ARG	A	150	31.652	41.781	25.154	1.00	52.52	A N
ATOM	196	C	ARG	A	150	34.322	47.829	22.440	1.00	47.01	A C
ATOM	197	O	ARG	A	150	34.703	47.296	21.397	1.00	47.88	A O
ATOM	198	N	GLU	A	151	35.042	48.730	23.093	1.00	49.42	A N
ATOM	199	CA	GLU	A	151	36.365	49.124	22.632	1.00	54.61	A C
ATOM	200	CB	GLU	A	151	36.848	50.346	23.426	1.00	56.69	A C
ATOM	201	CG	GLU	A	151	37.983	51.140	22.766	1.00	63.91	A C
ATOM	202	CD	GLU	A	151	39.363	50.535	22.995	1.00	66.90	A C
ATOM	203	OE1	GLU	A	151	39.845	50.581	24.151	1.00	67.65	A O
ATOM	204	OE2	GLU	A	151	39.967	50.018	22.024	1.00	69.20	A O
ATOM	205	C	GLU	A	151	37.265	47.917	22.871	1.00	56.41	A C
ATOM	206	O	GLU	A	151	37.304	47.384	23.975	1.00	56.29	A O
ATOM	207	N	LYS	A	152	37.963	47.471	21.830	1.00	59.00	A N
ATOM	208	CA	LYS	A	152	38.842	46.305	21.934	1.00	60.50	A C
ATOM	209	CB	LYS	A	152	39.626	46.114	20.630	1.00	61.26	A C
ATOM	210	CG	LYS	A	152	38.765	45.794	19.402	1.00	61.58	A C
ATOM	211	CD	LYS	A	152	39.643	45.531	18.171	1.00	62.51	A C
ATOM	212	CE	LYS	A	152	38.831	45.211	16.916	1.00	61.68	A C
ATOM	213	NZ	LYS	A	152	37.959	44.023	17.075	1.00	63.73	A N
ATOM	214	C	LYS	A	152	39.816	46.390	23.111	1.00	61.70	A C
ATOM	215	O	LYS	A	152	39.759	45.572	24.030	1.00	60.64	A O
ATOM	216	N	GLN	A	153	40.702	47.381	23.083	1.00	63.23	A N
ATOM	217	CA	GLN	A	153	41.689	47.562	24.145	1.00	66.35	A C
ATOM	218	CB	GLN	A	153	42.477	48.859	23.916	1.00	68.76	A C
ATOM	219	CG	GLN	A	153	43.247	48.912	22.597	1.00	72.76	A C
ATOM	220	CD	GLN	A	153	44.497	48.038	22.595	1.00	75.69	A C
ATOM	221	OE1	GLN	A	153	44.438	46.835	22.872	1.00	75.15	A O
ATOM	222	NE2	GLN	A	153	45.639	48.644	22.273	1.00	76.04	A N
ATOM	223	C	GLN	A	153	41.055	47.600	25.535	1.00	67.63	A C
ATOM	224	O	GLN	A	153	41.276	46.709	26.360	1.00	67.71	A O
ATOM	225	N	SER	A	154	40.265	48.642	25.776	1.00	67.64	A N
ATOM	226	CA	SER	A	154	39.592	48.858	27.054	1.00	68.46	A C
ATOM	227	CB	SER	A	154	38.963	50.253	27.067	1.00	68.69	A C
ATOM	228	OG	SER	A	154	38.180	50.435	28.231	1.00	72.14	A O
ATOM	229	C	SER	A	154	38.524	47.827	27.413	1.00	67.39	A C
ATOM	230	O	SER	A	154	38.422	47.404	28.562	1.00	66.91	A O
ATOM	231	N	LYS	A	155	37.722	47.447	26.426	1.00	66.94	A N
ATOM	232	CA	LYS	A	155	36.645	46.479	26.602	1.00	65.83	A C
ATOM	233	CB	LYS	A	155	37.166	45.229	27.310	1.00	66.50	A C
ATOM	234	CG	LYS	A	155	38.159	44.456	26.452	1.00	69.74	A C
ATOM	235	CD	LYS	A	155	38.437	43.070	26.992	1.00	70.98	A C
ATOM	236	CE	LYS	A	155	39.396	42.318	26.080	1.00	72.81	A C
ATOM	237	NZ	LYS	A	155	39.663	40.936	26.573	1.00	75.35	A N
ATOM	238	C	LYS	A	155	35.422	47.053	27.326	1.00	64.74	A C
ATOM	239	O	LYS	A	155	34.608	46.318	27.891	1.00	63.21	A O
ATOM	240	N	PHE	A	156	35.289	48.375	27.278	1.00	63.83	A N
ATOM	241	CA	PHE	A	156	34.162	49.061	27.901	1.00	61.40	A C
ATOM	242	CB	PHE	A	156	34.544	50.514	28.194	1.00	63.97	A C
ATOM	243	CG	PHE	A	156	33.478	51.290	28.911	1.00	68.01	A C
ATOM	244	CD1	PHE	A	156	32.956	50.832	30.121	1.00	69.99	A C
ATOM	245	CD2	PHE	A	156	33.004	52.490	28.387	1.00	68.86	A C
ATOM	246	CE1	PHE	A	156	31.975	51.559	30.800	1.00	70.97	A C

ATOM	247	CE2	PHE	A	156	32.026	53.224	29.055	1.00	69.64	A	C
ATOM	248	CZ	PHE	A	156	31.510	52.759	30.264	1.00	70.88	A	C
ATOM	249	C	PHE	A	156	32.963	49.013	26.946	1.00	57.88	A	C
ATOM	250	O	PHE	A	156	33.127	49.157	25.732	1.00	55.27	A	O
ATOM	251	N	ILE	A	157	31.768	48.799	27.498	1.00	53.85	A	N
ATOM	252	CA	ILE	A	157	30.542	48.730	26.701	1.00	50.05	A	C
ATOM	253	CB	ILE	A	157	29.434	47.949	27.459	1.00	50.70	A	C
ATOM	254	CG2	ILE	A	157	28.097	48.111	26.760	1.00	48.39	A	C
ATOM	255	CG1	ILE	A	157	29.800	46.464	27.545	1.00	51.64	A	C
ATOM	256	CD1	ILE	A	157	29.635	45.707	26.244	1.00	52.26	A	C
ATOM	257	C	ILE	A	157	30.020	50.130	26.353	1.00	47.74	A	C
ATOM	258	O	ILE	A	157	29.998	51.021	27.203	1.00	45.67	A	O
ATOM	259	N	LEU	A	158	29.609	50.308	25.097	1.00	44.24	A	N
ATOM	260	CA	LEU	A	158	29.079	51.586	24.618	1.00	43.05	A	C
ATOM	261	CB	LEU	A	158	30.229	52.539	24.251	1.00	42.08	A	C
ATOM	262	CG	LEU	A	158	31.339	52.029	23.327	1.00	45.57	A	C
ATOM	263	CD1	LEU	A	158	30.844	51.994	21.901	1.00	46.09	A	C
ATOM	264	CD2	LEU	A	158	32.566	52.940	23.435	1.00	46.27	A	C
ATOM	265	C	LEU	A	158	28.154	51.392	23.427	1.00	39.34	A	C
ATOM	266	O	LEU	A	158	27.861	50.269	23.036	1.00	38.00	A	O
ATOM	267	N	ALA	A	159	27.669	52.489	22.858	1.00	39.30	A	N
ATOM	268	CA	ALA	A	159	26.789	52.384	21.702	1.00	38.21	A	C
ATOM	269	CB	ALA	A	159	25.438	53.007	22.006	1.00	37.68	A	C
ATOM	270	C	ALA	A	159	27.443	53.082	20.525	1.00	38.81	A	C
ATOM	271	O	ALA	A	159	28.146	54.073	20.694	1.00	38.10	A	O
ATOM	272	N	LEU	A	160	27.221	52.556	19.329	1.00	39.75	A	N
ATOM	273	CA	LEU	A	160	27.806	53.152	18.145	1.00	39.68	A	C
ATOM	274	CB	LEU	A	160	28.793	52.175	17.503	1.00	41.87	A	C
ATOM	275	CG	LEU	A	160	29.841	52.748	16.543	1.00	44.90	A	C
ATOM	276	CD1	LEU	A	160	30.807	53.651	17.305	1.00	43.49	A	C
ATOM	277	CD2	LEU	A	160	30.602	51.604	15.885	1.00	44.40	A	C
ATOM	278	C	LEU	A	160	26.690	53.496	17.169	1.00	39.67	A	C
ATOM	279	O	LEU	A	160	26.005	52.610	16.666	1.00	39.99	A	O
ATOM	280	N	LYS	A	161	26.493	54.788	16.921	1.00	38.00	A	N
ATOM	281	CA	LYS	A	161	25.461	55.212	15.996	1.00	39.14	A	C
ATOM	282	CB	LYS	A	161	24.782	56.501	16.480	1.00	40.21	A	C
ATOM	283	CG	LYS	A	161	23.783	57.073	15.485	1.00	43.91	A	C
ATOM	284	CD	LYS	A	161	23.120	58.347	15.994	1.00	45.72	A	C
ATOM	285	CE	LYS	A	161	22.171	58.060	17.140	1.00	48.13	A	C
ATOM	286	NZ	LYS	A	161	21.511	59.299	17.670	1.00	52.12	A	N
ATOM	287	C	LYS	A	161	26.102	55.429	14.644	1.00	36.94	A	C
ATOM	288	O	LYS	A	161	26.961	56.294	14.485	1.00	35.11	A	O
ATOM	289	N	VAL	A	162	25.661	54.631	13.677	1.00	37.87	A	N
ATOM	290	CA	VAL	A	162	26.168	54.656	12.311	1.00	37.92	A	C
ATOM	291	CB	VAL	A	162	26.400	53.201	11.807	1.00	39.41	A	C
ATOM	292	CG1	VAL	A	162	27.179	53.214	10.506	1.00	37.99	A	C
ATOM	293	CG2	VAL	A	162	27.142	52.382	12.873	1.00	37.26	A	C
ATOM	294	C	VAL	A	162	25.180	55.362	11.368	1.00	39.49	A	C
ATOM	295	O	VAL	A	162	24.070	54.878	11.141	1.00	40.14	A	O
ATOM	296	N	LEU	A	163	25.595	56.500	10.817	1.00	39.18	A	N
ATOM	297	CA	LEU	A	163	24.757	57.277	9.907	1.00	42.61	A	C
ATOM	298	CB	LEU	A	163	24.659	58.726	10.400	1.00	43.27	A	C
ATOM	299	CG	LEU	A	163	23.621	59.124	11.457	1.00	42.79	A	C
ATOM	300	CD1	LEU	A	163	23.227	57.944	12.311	1.00	43.48	A	C
ATOM	301	CD2	LEU	A	163	24.201	60.246	12.313	1.00	43.16	A	C
ATOM	302	C	LEU	A	163	25.279	57.278	8.466	1.00	45.56	A	C
ATOM	303	O	LEU	A	163	26.462	57.515	8.228	1.00	43.94	A	O
ATOM	304	N	PHE	A	164	24.381	57.029	7.513	1.00	48.16	A	N
ATOM	305	CA	PHE	A	164	24.733	57.006	6.091	1.00	52.24	A	C
ATOM	306	CB	PHE	A	164	23.624	56.332	5.286	1.00	53.67	A	C
ATOM	307	CG	PHE	A	164	23.201	55.008	5.831	1.00	55.86	A	C
ATOM	308	CD1	PHE	A	164	21.865	54.625	5.781	1.00	56.34	A	C
ATOM	309	CD2	PHE	A	164	24.133	54.139	6.392	1.00	55.83	A	C
ATOM	310	CE1	PHE	A	164	21.460	53.393	6.286	1.00	58.23	A	C
ATOM	311	CE2	PHE	A	164	23.743	52.907	6.897	1.00	55.86	A	C
ATOM	312	CZ	PHE	A	164	22.404	52.530	6.846	1.00	58.79	A	C
ATOM	313	C	PHE	A	164	24.919	58.423	5.551	1.00	53.31	A	C
ATOM	314	O	PHE	A	164	24.022	59.262	5.676	1.00	51.66	A	O
ATOM	315	N	LYS	A	165	26.072	58.682	4.940	1.00	55.24	A	N
ATOM	316	CA	LYS	A	165	26.355	60.000	4.372	1.00	57.91	A	C
ATOM	317	CB	LYS	A	165	27.751	60.033	3.754	1.00	57.31	A	C
ATOM	318	CG	LYS	A	165	28.881	60.126	4.756	1.00	57.21	A	C

ATOM	319	CD	LYS	A	165	30.201	60.338	4.040	1.00	57.36	A C
ATOM	320	CE	LYS	A	165	31.340	60.528	5.018	1.00	58.00	A C
ATOM	321	NZ	LYS	A	165	32.638	60.675	4.309	1.00	60.01	A N
ATOM	322	C	LYS	A	165	25.340	60.392	3.306	1.00	59.50	A C
ATOM	323	O	LYS	A	165	24.971	61.559	3.194	1.00	59.56	A O
ATOM	324	N	ALA	A	166	24.894	59.407	2.534	1.00	62.03	A N
ATOM	325	CA	ALA	A	166	23.931	59.628	1.462	1.00	66.28	A C
ATOM	326	CB	ALA	A	166	23.673	58.319	0.728	1.00	65.88	A C
ATOM	327	C	ALA	A	166	22.606	60.229	1.939	1.00	69.38	A C
ATOM	328	O	ALA	A	166	21.706	60.485	1.132	1.00	69.73	A O
ATOM	329	N	GLN	A	167	22.486	60.447	3.246	1.00	70.89	A N
ATOM	330	CA	GLN	A	167	21.272	61.017	3.819	1.00	71.80	A C
ATOM	331	CB	GLN	A	167	20.686	60.063	4.856	1.00	73.19	A C
ATOM	332	CG	GLN	A	167	20.621	58.625	4.388	1.00	76.66	A C
ATOM	333	CD	GLN	A	167	19.769	58.453	3.152	1.00	79.08	A C
ATOM	334	OE1	GLN	A	167	19.772	57.390	2.527	1.00	80.82	A O
ATOM	335	NE2	GLN	A	167	19.025	59.497	2.792	1.00	80.53	A N
ATOM	336	C	GLN	A	167	21.597	62.352	4.477	1.00	72.50	A C
ATOM	337	O	GLN	A	167	20.884	63.336	4.298	1.00	71.35	A O
ATOM	338	N	LEU	A	168	22.676	62.379	5.247	1.00	73.59	A N
ATOM	339	CA	LEU	A	168	23.082	63.602	5.912	1.00	76.12	A C
ATOM	340	CB	LEU	A	168	24.460	63.421	6.552	1.00	74.15	A C
ATOM	341	CG	LEU	A	168	24.547	62.317	7.612	1.00	73.50	A C
ATOM	342	CD1	LEU	A	168	25.979	62.150	8.066	1.00	72.46	A C
ATOM	343	CD2	LEU	A	168	23.656	62.665	8.789	1.00	72.72	A C
ATOM	344	C	LEU	A	168	23.112	64.728	4.881	1.00	78.84	A C
ATOM	345	O	LEU	A	168	22.254	65.610	4.896	1.00	79.50	A O
ATOM	346	N	GLU	A	169	24.086	64.681	3.976	1.00	81.12	A N
ATOM	347	CA	GLU	A	169	24.228	65.697	2.936	1.00	83.10	A C
ATOM	348	CB	GLU	A	169	25.344	65.296	1.971	1.00	83.78	A C
ATOM	349	CG	GLU	A	169	25.096	63.979	1.255	1.00	85.16	A C
ATOM	350	CD	GLU	A	169	26.298	63.510	0.457	1.00	86.11	A C
ATOM	351	OE1	GLU	A	169	27.361	63.266	1.068	1.00	85.05	A O
ATOM	352	OE2	GLU	A	169	26.179	63.387	-0.781	1.00	87.77	A O
ATOM	353	C	GLU	A	169	22.924	65.891	2.164	1.00	83.83	A C
ATOM	354	O	GLU	A	169	22.541	67.018	1.840	1.00	83.53	A O
ATOM	355	N	LYS	A	170	22.250	64.782	1.878	1.00	84.15	A N
ATOM	356	CA	LYS	A	170	20.985	64.794	1.149	1.00	85.24	A C
ATOM	357	CB	LYS	A	170	20.809	63.467	0.411	1.00	84.77	A C
ATOM	358	CG	LYS	A	170	19.407	63.207	-0.112	1.00	84.91	A C
ATOM	359	CD	LYS	A	170	19.271	61.764	-0.560	1.00	84.46	A C
ATOM	360	CE	LYS	A	170	17.863	61.447	-1.022	1.00	84.75	A C
ATOM	361	NZ	LYS	A	170	17.754	60.021	-1.434	1.00	84.95	A N
ATOM	362	C	LYS	A	170	19.797	65.020	2.085	1.00	86.98	A C
ATOM	363	O	LYS	A	170	19.175	64.058	2.547	1.00	88.55	A O
ATOM	364	N	ALA	A	171	19.495	66.291	2.353	1.00	86.65	A N
ATOM	365	CA	ALA	A	171	18.388	66.702	3.222	1.00	86.88	A C
ATOM	366	CB	ALA	A	171	17.388	65.561	3.418	1.00	86.71	A C
ATOM	367	C	ALA	A	171	18.877	67.194	4.577	1.00	86.86	A C
ATOM	368	O	ALA	A	171	19.133	68.386	4.754	1.00	86.68	A O
ATOM	369	N	GLY	A	172	18.993	66.275	5.533	1.00	86.88	A N
ATOM	370	CA	GLY	A	172	19.449	66.635	6.866	1.00	86.26	A C
ATOM	371	C	GLY	A	172	20.858	67.190	6.837	1.00	86.14	A C
ATOM	372	O	GLY	A	172	21.659	66.924	7.735	1.00	86.73	A O
ATOM	373	N	VAL	A	173	21.141	67.967	5.793	1.00	85.19	A N
ATOM	374	CA	VAL	A	173	22.437	68.593	5.564	1.00	83.10	A C
ATOM	375	CB	VAL	A	173	22.280	70.107	5.336	1.00	82.25	A C
ATOM	376	CG1	VAL	A	173	23.622	70.720	4.988	1.00	79.89	A C
ATOM	377	CG2	VAL	A	173	21.276	70.355	4.223	1.00	82.16	A C
ATOM	378	C	VAL	A	173	23.450	68.364	6.678	1.00	82.27	A C
ATOM	379	O	VAL	A	173	23.174	68.599	7.857	1.00	82.63	A O
ATOM	380	N	GLU	A	174	24.629	67.897	6.289	1.00	80.75	A N
ATOM	381	CA	GLU	A	174	25.690	67.639	7.242	1.00	79.61	A C
ATOM	382	CB	GLU	A	174	26.984	67.310	6.492	1.00	80.39	A C
ATOM	383	CG	GLU	A	174	28.221	67.233	7.369	1.00	81.70	A C
ATOM	384	CD	GLU	A	174	28.904	68.577	7.535	1.00	83.27	A C
ATOM	385	OE1	GLU	A	174	29.877	68.658	8.314	1.00	83.32	A O
ATOM	386	OE2	GLU	A	174	28.474	69.552	6.879	1.00	83.99	A O
ATOM	387	C	GLU	A	174	25.886	68.848	8.151	1.00	78.82	A C
ATOM	388	O	GLU	A	174	26.258	68.701	9.313	1.00	78.22	A O
ATOM	389	N	HIS	A	175	25.618	70.038	7.615	1.00	78.24	A N
ATOM	390	CA	HIS	A	175	25.770	71.285	8.363	1.00	77.47	A C

ATOM	391	CB	HIS	A	175	25.205	72.463	7.562	1.00	76.98	A	C
ATOM	392	CG	HIS	A	175	25.859	72.663	6.231	1.00	77.17	A	C
ATOM	393	CD2	HIS	A	175	26.828	71.962	5.597	1.00	76.90	A	C
ATOM	394	ND1	HIS	A	175	25.506	73.687	5.378	1.00	77.46	A	N
ATOM	395	CE1	HIS	A	175	26.229	73.607	4.275	1.00	77.33	A	C
ATOM	396	NE2	HIS	A	175	27.039	72.568	4.382	1.00	77.65	A	N
ATOM	397	C	HIS	A	175	25.073	71.223	9.716	1.00	76.86	A	C
ATOM	398	O	HIS	A	175	25.709	71.382	10.756	1.00	74.77	A	O
ATOM	399	N	GLN	A	176	23.761	70.998	9.684	1.00	77.67	A	N
ATOM	400	CA	GLN	A	176	22.946	70.907	10.893	1.00	79.14	A	C
ATOM	401	CB	GLN	A	176	21.495	70.583	10.517	1.00	79.88	A	C
ATOM	402	CG	GLN	A	176	20.643	70.082	11.673	1.00	81.72	A	C
ATOM	403	CD	GLN	A	176	19.203	69.804	11.272	1.00	83.00	A	C
ATOM	404	OE1	GLN	A	176	18.444	69.197	12.028	1.00	82.78	A	O
ATOM	405	NE2	GLN	A	176	18.818	70.257	10.081	1.00	83.25	A	N
ATOM	406	C	GLN	A	176	23.459	69.858	11.873	1.00	79.66	A	C
ATOM	407	O	GLN	A	176	23.533	70.103	13.079	1.00	78.29	A	O
ATOM	408	N	ALA	A	177	23.816	68.689	11.348	1.00	81.28	A	N
ATOM	409	CA	ALA	A	177	24.305	67.596	12.178	1.00	82.55	A	C
ATOM	410	CB	ALA	A	177	23.604	66.305	11.786	1.00	83.52	A	C
ATOM	411	C	ALA	A	177	25.814	67.399	12.113	1.00	83.96	A	C
ATOM	412	O	ALA	A	177	26.284	66.312	11.767	1.00	85.89	A	O
ATOM	413	N	ARG	A	178	26.575	68.438	12.447	1.00	84.10	A	N
ATOM	414	CA	ARG	A	178	28.029	68.327	12.426	1.00	84.25	A	C
ATOM	415	CB	ARG	A	178	28.612	68.952	11.160	1.00	83.50	A	C
ATOM	416	CG	ARG	A	178	30.132	69.065	11.216	1.00	84.36	A	C
ATOM	417	CD	ARG	A	178	30.782	67.748	11.659	1.00	83.46	A	C
ATOM	418	NE	ARG	A	178	32.208	67.902	11.948	1.00	81.99	A	N
ATOM	419	CZ	ARG	A	178	32.704	68.564	12.990	1.00	79.87	A	C
ATOM	420	NH1	ARG	A	178	31.897	69.144	13.867	1.00	78.59	A	N
ATOM	421	NH2	ARG	A	178	34.017	68.652	13.149	1.00	78.59	A	N
ATOM	422	C	ARG	A	178	28.735	68.923	13.639	1.00	83.89	A	C
ATOM	423	O	ARG	A	178	29.075	68.199	14.576	1.00	84.19	A	O
ATOM	424	N	ALA	A	179	28.971	70.234	13.610	1.00	83.02	A	N
ATOM	425	CA	ALA	A	179	29.657	70.913	14.711	1.00	81.63	A	C
ATOM	426	CB	ALA	A	179	29.708	72.420	14.457	1.00	82.10	A	C
ATOM	427	C	ALA	A	179	28.928	70.622	16.010	1.00	80.48	A	C
ATOM	428	O	ALA	A	179	29.497	70.733	17.102	1.00	79.55	A	O
ATOM	429	N	GLU	A	180	27.658	70.253	15.869	1.00	79.39	A	N
ATOM	430	CA	GLU	A	180	26.815	69.908	17.002	1.00	78.29	A	C
ATOM	431	CB	GLU	A	180	25.389	69.647	16.521	1.00	78.71	A	C
ATOM	432	CG	GLU	A	180	24.543	70.903	16.382	1.00	81.63	A	C
ATOM	433	CD	GLU	A	180	25.322	72.098	15.848	1.00	83.43	A	C
ATOM	434	OE1	GLU	A	180	26.170	72.639	16.591	1.00	84.35	A	O
ATOM	435	OE2	GLU	A	180	25.088	72.499	14.686	1.00	84.07	A	O
ATOM	436	C	GLU	A	180	27.382	68.681	17.713	1.00	75.99	A	C
ATOM	437	O	GLU	A	180	26.838	68.226	18.720	1.00	75.13	A	O
ATOM	438	N	VAL	A	181	28.471	68.146	17.165	1.00	73.03	A	N
ATOM	439	CA	VAL	A	181	29.148	66.999	17.757	1.00	70.84	A	C
ATOM	440	CB	VAL	A	181	29.938	66.175	16.706	1.00	70.79	A	C
ATOM	441	CG1	VAL	A	181	30.861	65.180	17.409	1.00	69.55	A	C
ATOM	442	CG2	VAL	A	181	28.973	65.433	15.791	1.00	69.51	A	C
ATOM	443	C	VAL	A	181	30.128	67.585	18.758	1.00	69.44	A	C
ATOM	444	O	VAL	A	181	30.351	67.026	19.831	1.00	69.27	A	O
ATOM	445	N	ALA	A	182	30.707	68.724	18.392	1.00	68.30	A	N
ATOM	446	CA	ALA	A	182	31.654	69.416	19.259	1.00	66.45	A	C
ATOM	447	CB	ALA	A	182	32.419	70.483	18.469	1.00	67.64	A	C
ATOM	448	C	ALA	A	182	30.900	70.057	20.425	1.00	64.52	A	C
ATOM	449	O	ALA	A	182	31.368	70.013	21.567	1.00	64.11	A	O
ATOM	450	N	ILE	A	183	29.737	70.649	20.146	1.00	59.92	A	N
ATOM	451	CA	ILE	A	183	28.969	71.262	21.222	1.00	59.47	A	C
ATOM	452	CB	ILE	A	183	27.772	72.131	20.710	1.00	60.11	A	C
ATOM	453	CG2	ILE	A	183	28.277	73.193	19.744	1.00	60.37	A	C
ATOM	454	CG1	ILE	A	183	26.705	71.251	20.053	1.00	60.21	A	C
ATOM	455	CD1	ILE	A	183	25.391	71.971	19.783	1.00	60.28	A	C
ATOM	456	C	ILE	A	183	28.437	70.164	22.140	1.00	56.99	A	C
ATOM	457	O	ILE	A	183	28.617	70.229	23.350	1.00	56.38	A	O
ATOM	458	N	GLN	A	184	27.799	69.150	21.562	1.00	56.33	A	N
ATOM	459	CA	GLN	A	184	27.264	68.045	22.352	1.00	56.17	A	C
ATOM	460	CB	GLN	A	184	26.552	67.026	21.458	1.00	57.52	A	C
ATOM	461	CG	GLN	A	184	25.670	66.045	22.228	1.00	61.39	A	C
ATOM	462	CD	GLN	A	184	24.324	66.650	22.615	1.00	64.82	A	C

ATOM	463	OE1	GLN	A	184	23.672	66.213	23.570	1.00	62.62	A	O
ATOM	464	NE2	GLN	A	184	23.897	67.654	21.857	1.00	65.33	A	N
ATOM	465	C	GLN	A	184	28.381	67.342	23.124	1.00	54.27	A	C
ATOM	466	O	GLN	A	184	28.236	67.057	24.308	1.00	53.30	A	O
ATOM	467	N	SER	A	185	29.498	67.076	22.458	1.00	53.49	A	N
ATOM	468	CA	SER	A	185	30.621	66.401	23.106	1.00	55.92	A	C
ATOM	469	CB	SER	A	185	31.786	66.247	22.128	1.00	56.01	A	C
ATOM	470	OG	SER	A	185	32.335	67.510	21.797	1.00	55.72	A	O
ATOM	471	C	SER	A	185	31.115	67.152	24.342	1.00	56.22	A	C
ATOM	472	O	SER	A	185	31.636	66.551	25.281	1.00	55.88	A	O
ATOM	473	N	HIS	A	186	30.945	68.467	24.341	1.00	56.92	A	N
ATOM	474	CA	HIS	A	186	31.399	69.281	25.460	1.00	58.35	A	C
ATOM	475	CB	HIS	A	186	31.765	70.676	24.953	1.00	61.17	A	C
ATOM	476	CG	HIS	A	186	32.936	70.683	24.017	1.00	64.95	A	C
ATOM	477	CD2	HIS	A	186	33.986	69.834	23.898	1.00	65.77	A	C
ATOM	478	ND1	HIS	A	186	33.120	71.656	23.056	1.00	66.54	A	N
ATOM	479	CE1	HIS	A	186	34.231	71.404	22.386	1.00	66.45	A	C
ATOM	480	NE2	HIS	A	186	34.775	70.305	22.877	1.00	66.45	A	N
ATOM	481	C	HIS	A	186	30.399	69.359	26.610	1.00	56.48	A	C
ATOM	482	O	HIS	A	186	30.615	70.079	27.583	1.00	57.86	A	O
ATOM	483	N	LEU	A	187	29.304	68.614	26.496	1.00	53.92	A	N
ATOM	484	CA	LEU	A	187	28.296	68.580	27.543	1.00	52.14	A	C
ATOM	485	CB	LEU	A	187	26.900	68.410	26.935	1.00	51.03	A	C
ATOM	486	CG	LEU	A	187	26.067	69.660	26.626	1.00	52.63	A	C
ATOM	487	CD1	LEU	A	187	26.958	70.858	26.344	1.00	52.17	A	C
ATOM	488	CD2	LEU	A	187	25.158	69.365	25.444	1.00	51.26	A	C
ATOM	489	C	LEU	A	187	28.619	67.401	28.454	1.00	51.97	A	C
ATOM	490	O	LEU	A	187	28.631	66.256	28.010	1.00	51.83	A	O
ATOM	491	N	ARG	A	188	28.891	67.682	29.724	1.00	50.85	A	N
ATOM	492	CA	ARG	A	188	29.213	66.626	30.676	1.00	49.45	A	C
ATOM	493	CB	ARG	A	188	30.703	66.670	31.026	1.00	52.24	A	C
ATOM	494	CG	ARG	A	188	31.595	66.327	29.838	1.00	56.65	A	C
ATOM	495	CD	ARG	A	188	33.042	66.111	30.252	1.00	61.31	A	C
ATOM	496	NE	ARG	A	188	33.881	65.699	29.126	1.00	64.86	A	N
ATOM	497	CZ	ARG	A	188	34.195	66.477	28.092	1.00	65.93	A	C
ATOM	498	NH1	ARG	A	188	33.744	67.725	28.028	1.00	67.33	A	N
ATOM	499	NH2	ARG	A	188	34.959	66.007	27.115	1.00	66.11	A	N
ATOM	500	C	ARG	A	188	28.356	66.746	31.923	1.00	47.99	A	C
ATOM	501	O	ARG	A	188	28.619	67.561	32.813	1.00	47.40	A	O
ATOM	502	N	HIS	A	189	27.323	65.913	31.981	1.00	46.41	A	N
ATOM	503	CA	HIS	A	189	26.387	65.939	33.095	1.00	43.42	A	C
ATOM	504	CB	HIS	A	189	25.288	66.961	32.775	1.00	39.93	A	C
ATOM	505	CG	HIS	A	189	24.371	67.255	33.918	1.00	37.78	A	C
ATOM	506	CD2	HIS	A	189	24.342	68.289	34.793	1.00	37.18	A	C
ATOM	507	ND1	HIS	A	189	23.322	66.431	34.261	1.00	38.04	A	N
ATOM	508	CE1	HIS	A	189	22.681	66.948	35.296	1.00	40.74	A	C
ATOM	509	NE2	HIS	A	189	23.281	68.076	35.637	1.00	38.70	A	N
ATOM	510	C	HIS	A	189	25.794	64.546	33.314	1.00	42.45	A	C
ATOM	511	O	HIS	A	189	25.585	63.799	32.367	1.00	43.83	A	O
ATOM	512	N	PRO	A	190	25.539	64.171	34.576	1.00	41.87	A	N
ATOM	513	CD	PRO	A	190	25.811	64.893	35.829	1.00	41.35	A	C
ATOM	514	CA	PRO	A	190	24.970	62.850	34.851	1.00	40.95	A	C
ATOM	515	CB	PRO	A	190	24.878	62.820	36.378	1.00	40.22	A	C
ATOM	516	CG	PRO	A	190	24.803	64.267	36.758	1.00	43.23	A	C
ATOM	517	C	PRO	A	190	23.626	62.591	34.178	1.00	40.60	A	C
ATOM	518	O	PRO	A	190	23.260	61.442	33.931	1.00	40.06	A	O
ATOM	519	N	ASN	A	191	22.886	63.650	33.865	1.00	39.67	A	N
ATOM	520	CA	ASN	A	191	21.594	63.451	33.237	1.00	37.85	A	C
ATOM	521	CB	ASN	A	191	20.532	64.244	34.003	1.00	39.49	A	C
ATOM	522	CG	ASN	A	191	20.373	63.762	35.446	1.00	37.64	A	C
ATOM	523	OD1	ASN	A	191	20.013	62.606	35.695	1.00	38.24	A	O
ATOM	524	ND2	ASN	A	191	20.647	64.645	36.397	1.00	35.93	A	N
ATOM	525	C	ASN	A	191	21.570	63.766	31.735	1.00	37.60	A	C
ATOM	526	O	ASN	A	191	20.518	64.003	31.150	1.00	36.22	A	O
ATOM	527	N	ILE	A	192	22.741	63.776	31.112	1.00	37.28	A	N
ATOM	528	CA	ILE	A	192	22.829	64.006	29.673	1.00	38.27	A	C
ATOM	529	CB	ILE	A	192	23.511	65.351	29.316	1.00	38.46	A	C
ATOM	530	CG2	ILE	A	192	23.623	65.488	27.795	1.00	35.81	A	C
ATOM	531	CG1	ILE	A	192	22.689	66.516	29.867	1.00	41.28	A	C
ATOM	532	CD1	ILE	A	192	23.199	67.881	29.476	1.00	38.83	A	C
ATOM	533	C	ILE	A	192	23.672	62.881	29.108	1.00	38.70	A	C
ATOM	534	O	ILE	A	192	24.772	62.629	29.597	1.00	38.53	A	O

ATOM	535	N	LEU	A	193	23.153	62.195	28.095	1.00	40.02	A	N
ATOM	536	CA	LEU	A	193	23.884	61.094	27.477	1.00	39.54	A	C
ATOM	537	CB	LEU	A	193	23.099	60.525	26.299	1.00	38.70	A	C
ATOM	538	CG	LEU	A	193	23.577	59.164	25.775	1.00	38.41	A	C
ATOM	539	CD1	LEU	A	193	23.122	58.073	26.751	1.00	35.03	A	C
ATOM	540	CD2	LEU	A	193	22.995	58.913	24.380	1.00	34.30	A	C
ATOM	541	C	LEU	A	193	25.211	61.630	26.973	1.00	40.55	A	C
ATOM	542	O	LEU	A	193	25.245	62.660	26.302	1.00	42.56	A	O
ATOM	543	N	ARG	A	194	26.308	60.947	27.282	1.00	40.25	A	N
ATOM	544	CA	ARG	A	194	27.593	61.436	26.820	1.00	41.82	A	C
ATOM	545	CB	ARG	A	194	28.728	61.018	27.756	1.00	43.59	A	C
ATOM	546	CG	ARG	A	194	30.023	61.749	27.418	1.00	49.64	A	C
ATOM	547	CD	ARG	A	194	31.216	61.273	28.217	1.00	56.35	A	C
ATOM	548	NE	ARG	A	194	32.436	62.006	27.871	1.00	60.72	A	N
ATOM	549	CZ	ARG	A	194	33.658	61.677	28.291	1.00	64.00	A	C
ATOM	550	NH1	ARG	A	194	33.834	60.621	29.076	1.00	64.55	A	N
ATOM	551	NH2	ARG	A	194	34.708	62.403	27.924	1.00	65.94	A	N
ATOM	552	C	ARG	A	194	27.957	61.023	25.401	1.00	42.36	A	C
ATOM	553	O	ARG	A	194	27.723	59.887	24.974	1.00	41.77	A	O
ATOM	554	N	LEU	A	195	28.517	61.981	24.671	1.00	41.98	A	N
ATOM	555	CA	LEU	A	195	28.981	61.763	23.308	1.00	43.72	A	C
ATOM	556	CB	LEU	A	195	28.538	62.912	22.395	1.00	42.46	A	C
ATOM	557	CG	LEU	A	195	28.545	62.694	20.878	1.00	46.89	A	C
ATOM	558	CD1	LEU	A	195	28.063	63.967	20.193	1.00	48.66	A	C
ATOM	559	CD2	LEU	A	195	29.926	62.338	20.395	1.00	45.85	A	C
ATOM	560	C	LEU	A	195	30.491	61.790	23.493	1.00	43.63	A	C
ATOM	561	O	LEU	A	195	31.061	62.851	23.722	1.00	45.28	A	O
ATOM	562	N	TYR	A	196	31.123	60.622	23.436	1.00	42.73	A	N
ATOM	563	CA	TYR	A	196	32.566	60.518	23.618	1.00	44.78	A	C
ATOM	564	CB	TYR	A	196	32.980	59.061	23.844	1.00	46.97	A	C
ATOM	565	CG	TYR	A	196	32.399	58.427	25.085	1.00	50.10	A	C
ATOM	566	CD1	TYR	A	196	31.409	57.452	24.996	1.00	50.68	A	C
ATOM	567	CE1	TYR	A	196	30.888	56.846	26.139	1.00	52.33	A	C
ATOM	568	CD2	TYR	A	196	32.853	58.786	26.352	1.00	51.97	A	C
ATOM	569	CE2	TYR	A	196	32.338	58.187	27.504	1.00	52.17	A	C
ATOM	570	CZ	TYR	A	196	31.358	57.220	27.389	1.00	54.59	A	C
ATOM	571	OH	TYR	A	196	30.844	56.626	28.525	1.00	57.15	A	O
ATOM	572	C	TYR	A	196	33.356	61.070	22.443	1.00	44.49	A	C
ATOM	573	O	TYR	A	196	34.445	61.604	22.622	1.00	45.61	A	O
ATOM	574	N	GLY	A	197	32.819	60.932	21.240	1.00	44.09	A	N
ATOM	575	CA	GLY	A	197	33.517	61.441	20.074	1.00	43.41	A	C
ATOM	576	C	GLY	A	197	32.913	60.907	18.797	1.00	43.77	A	C
ATOM	577	O	GLY	A	197	31.804	60.380	18.802	1.00	43.31	A	O
ATOM	578	N	TYR	A	198	33.633	61.044	17.694	1.00	44.25	A	N
ATOM	579	CA	TYR	A	198	33.127	60.551	16.425	1.00	45.18	A	C
ATOM	580	CB	TYR	A	198	32.041	61.491	15.889	1.00	44.33	A	C
ATOM	581	CG	TYR	A	198	32.571	62.592	14.997	1.00	55.20	A	C
ATOM	582	CD1	TYR	A	198	33.310	63.653	15.520	1.00	57.66	A	C
ATOM	583	CE1	TYR	A	198	33.845	64.638	14.688	1.00	59.20	A	C
ATOM	584	CD2	TYR	A	198	32.375	62.543	13.618	1.00	58.31	A	C
ATOM	585	CE2	TYR	A	198	32.904	63.521	12.775	1.00	60.71	A	C
ATOM	586	CZ	TYR	A	198	33.640	64.561	13.315	1.00	60.83	A	C
ATOM	587	OH	TYR	A	198	34.190	65.505	12.472	1.00	62.06	A	O
ATOM	588	C	TYR	A	198	34.235	60.408	15.382	1.00	43.11	A	C
ATOM	589	O	TYR	A	198	35.344	60.925	15.553	1.00	39.29	A	O
ATOM	590	N	PHE	A	199	33.913	59.695	14.307	1.00	41.05	A	N
ATOM	591	CA	PHE	A	199	34.834	59.483	13.194	1.00	42.76	A	C
ATOM	592	CB	PHE	A	199	35.884	58.405	13.540	1.00	41.19	A	C
ATOM	593	CG	PHE	A	199	35.308	57.040	13.853	1.00	42.02	A	C
ATOM	594	CD1	PHE	A	199	35.100	56.105	12.842	1.00	42.90	A	C
ATOM	595	CD2	PHE	A	199	35.025	56.677	15.162	1.00	40.34	A	C
ATOM	596	CE1	PHE	A	199	34.623	54.822	13.129	1.00	40.61	A	C
ATOM	597	CE2	PHE	A	199	34.545	55.394	15.465	1.00	43.97	A	C
ATOM	598	CZ	PHE	A	199	34.347	54.464	14.441	1.00	41.24	A	C
ATOM	599	C	PHE	A	199	34.012	59.104	11.964	1.00	42.14	A	C
ATOM	600	O	PHE	A	199	32.807	58.881	12.068	1.00	42.73	A	O
ATOM	601	N	HIS	A	200	34.647	59.068	10.800	1.00	42.87	A	N
ATOM	602	CA	HIS	A	200	33.946	58.732	9.570	1.00	44.89	A	C
ATOM	603	CB	HIS	A	200	33.493	60.002	8.856	1.00	46.96	A	C
ATOM	604	CG	HIS	A	200	34.610	60.727	8.170	1.00	51.07	A	C
ATOM	605	CD2	HIS	A	200	34.913	60.863	6.856	1.00	52.59	A	C
ATOM	606	ND1	HIS	A	200	35.616	61.370	8.862	1.00	53.07	A	N

ATOM	607	CE1	HIS	A 200	36.489	61.870	8.005	1.00	53.71	A	C
ATOM	608	NE2	HIS	A 200	36.087	61.576	6.781	1.00	52.64	A	N
ATOM	609	C	HIS	A 200	34.838	57.969	8.597	1.00	44.12	A	C
ATOM	610	O	HIS	A 200	36.041	57.819	8.813	1.00	43.09	A	O
ATOM	611	N	ASP	A 201	34.214	57.494	7.525	1.00	42.67	A	N
ATOM	612	CA	ASP	A 201	34.910	56.818	6.442	1.00	44.38	A	C
ATOM	613	CB	ASP	A 201	34.819	55.281	6.545	1.00	44.11	A	C
ATOM	614	CG	ASP	A 201	33.399	54.766	6.553	1.00	43.31	A	C
ATOM	615	OD1	ASP	A 201	32.535	55.361	5.881	1.00	46.12	A	O
ATOM	616	OD2	ASP	A 201	33.152	53.742	7.222	1.00	45.46	A	O
ATOM	617	C	ASP	A 201	34.260	57.325	5.153	1.00	44.18	A	C
ATOM	618	O	ASP	A 201	33.535	58.322	5.166	1.00	42.40	A	O
ATOM	619	N	ALA	A 202	34.515	56.642	4.049	1.00	44.77	A	N
ATOM	620	CA	ALA	A 202	33.981	57.044	2.755	1.00	45.80	A	C
ATOM	621	CB	ALA	A 202	34.409	56.028	1.687	1.00	44.78	A	C
ATOM	622	C	ALA	A 202	32.470	57.227	2.696	1.00	46.73	A	C
ATOM	623	O	ALA	A 202	31.982	58.209	2.122	1.00	46.56	A	O
ATOM	624	N	THR	A 203	31.736	56.291	3.297	1.00	45.01	A	N
ATOM	625	CA	THR	A 203	30.282	56.318	3.245	1.00	45.70	A	C
ATOM	626	CB	THR	A 203	29.761	55.004	2.628	1.00	47.92	A	C
ATOM	627	OG1	THR	A 203	29.962	53.934	3.565	1.00	50.55	A	O
ATOM	628	CG2	THR	A 203	30.525	54.669	1.350	1.00	46.84	A	C
ATOM	629	C	THR	A 203	29.503	56.536	4.548	1.00	46.72	A	C
ATOM	630	O	THR	A 203	28.281	56.715	4.506	1.00	46.89	A	O
ATOM	631	N	ARG	A 204	30.170	56.528	5.699	1.00	43.86	A	N
ATOM	632	CA	ARG	A 204	29.424	56.680	6.948	1.00	41.61	A	C
ATOM	633	CB	ARG	A 204	29.167	55.300	7.577	1.00	42.57	A	C
ATOM	634	CG	ARG	A 204	28.645	54.199	6.646	1.00	45.37	A	C
ATOM	635	CD	ARG	A 204	28.299	52.983	7.491	1.00	52.00	A	C
ATOM	636	NE	ARG	A 204	28.122	51.719	6.769	1.00	59.45	A	N
ATOM	637	CZ	ARG	A 204	27.200	51.489	5.838	1.00	60.63	A	C
ATOM	638	NH1	ARG	A 204	26.350	52.439	5.480	1.00	63.62	A	N
ATOM	639	NH2	ARG	A 204	27.106	50.287	5.286	1.00	64.09	A	N
ATOM	640	C	ARG	A 204	30.073	57.564	8.010	1.00	39.60	A	C
ATOM	641	O	ARG	A 204	31.273	57.839	7.968	1.00	38.12	A	O
ATOM	642	N	VAL	A 205	29.249	57.993	8.967	1.00	38.69	A	N
ATOM	643	CA	VAL	A 205	29.684	58.807	10.098	1.00	36.15	A	C
ATOM	644	CB	VAL	A 205	28.872	60.127	10.202	1.00	39.01	A	C
ATOM	645	CG1	VAL	A 205	29.345	60.924	11.406	1.00	37.93	A	C
ATOM	646	CG2	VAL	A 205	29.031	60.957	8.919	1.00	36.49	A	C
ATOM	647	C	VAL	A 205	29.419	57.954	11.344	1.00	36.45	A	C
ATOM	648	O	VAL	A 205	28.365	57.331	11.457	1.00	36.62	A	O
ATOM	649	N	TYR	A 206	30.367	57.911	12.271	1.00	35.58	A	N
ATOM	650	CA	TYR	A 206	30.185	57.100	13.470	1.00	39.37	A	C
ATOM	651	CB	TYR	A 206	31.254	55.996	13.533	1.00	40.23	A	C
ATOM	652	CG	TYR	A 206	31.301	55.101	12.314	1.00	40.95	A	C
ATOM	653	CD1	TYR	A 206	31.811	55.565	11.101	1.00	43.93	A	C
ATOM	654	CE1	TYR	A 206	31.859	54.741	9.973	1.00	43.38	A	C
ATOM	655	CD2	TYR	A 206	30.836	53.784	12.372	1.00	43.86	A	C
ATOM	656	CE2	TYR	A 206	30.882	52.949	11.252	1.00	42.92	A	C
ATOM	657	CZ	TYR	A 206	31.394	53.436	10.057	1.00	43.76	A	C
ATOM	658	OH	TYR	A 206	31.433	52.623	8.946	1.00	45.92	A	O
ATOM	659	C	TYR	A 206	30.226	57.915	14.760	1.00	38.58	A	C
ATOM	660	O	TYR	A 206	31.200	58.604	15.045	1.00	40.46	A	O
ATOM	661	N	LEU	A 207	29.163	57.823	15.544	1.00	37.67	A	N
ATOM	662	CA	LEU	A 207	29.098	58.545	16.806	1.00	35.63	A	C
ATOM	663	CB	LEU	A 207	27.735	59.232	16.928	1.00	35.79	A	C
ATOM	664	CG	LEU	A 207	27.388	60.127	15.729	1.00	37.16	A	C
ATOM	665	CD1	LEU	A 207	25.985	60.681	15.899	1.00	37.87	A	C
ATOM	666	CD2	LEU	A 207	28.409	61.256	15.606	1.00	33.68	A	C
ATOM	667	C	LEU	A 207	29.314	57.561	17.955	1.00	33.49	A	C
ATOM	668	O	LEU	A 207	28.624	56.556	18.044	1.00	32.51	A	O
ATOM	669	N	ILE	A 208	30.276	57.858	18.826	1.00	31.11	A	N
ATOM	670	CA	ILE	A 208	30.592	56.997	19.961	1.00	32.62	A	C
ATOM	671	CB	ILE	A 208	32.094	57.029	20.266	1.00	31.85	A	C
ATOM	672	CG2	ILE	A 208	32.423	55.991	21.298	1.00	29.97	A	C
ATOM	673	CG1	ILE	A 208	32.889	56.759	18.983	1.00	34.87	A	C
ATOM	674	CD1	ILE	A 208	34.370	57.064	19.111	1.00	34.66	A	C
ATOM	675	C	ILE	A 208	29.827	57.494	21.185	1.00	33.51	A	C
ATOM	676	O	ILE	A 208	30.226	58.470	21.823	1.00	33.57	A	O
ATOM	677	N	LEU	A 209	28.747	56.794	21.515	1.00	32.77	A	N
ATOM	678	CA	LEU	A 209	27.867	57.173	22.613	1.00	33.70	A	C

ATOM	679	CB	LEU	A	209	26.413	57.171	22.104	1.00	31.78	A	C
ATOM	680	CG	LEU	A	209	26.089	58.037	20.880	1.00	31.51	A	C
ATOM	681	CD1	LEU	A	209	24.794	57.580	20.244	1.00	32.48	A	C
ATOM	682	CD2	LEU	A	209	26.011	59.504	21.295	1.00	32.98	A	C
ATOM	683	C	LEU	A	209	27.933	56.314	23.878	1.00	34.77	A	C
ATOM	684	O	LEU	A	209	28.326	55.151	23.842	1.00	35.59	A	O
ATOM	685	N	GLU	A	210	27.529	56.917	24.993	1.00	35.23	A	N
ATOM	686	CA	GLU	A	210	27.443	56.237	26.282	1.00	34.76	A	C
ATOM	687	CB	GLU	A	210	27.107	57.260	27.371	1.00	36.80	A	C
ATOM	688	CG	GLU	A	210	26.610	56.678	28.686	1.00	37.86	A	C
ATOM	689	CD	GLU	A	210	26.086	57.752	29.637	1.00	39.64	A	C
ATOM	690	OE1	GLU	A	210	25.525	57.394	30.691	1.00	38.77	A	O
ATOM	691	OE2	GLU	A	210	26.237	58.957	29.334	1.00	41.10	A	O
ATOM	692	C	GLU	A	210	26.269	55.281	26.102	1.00	34.26	A	C
ATOM	693	O	GLU	A	210	25.304	55.624	25.417	1.00	33.07	A	O
ATOM	694	N	TYR	A	211	26.334	54.091	26.699	1.00	34.30	A	N
ATOM	695	CA	TYR	A	211	25.234	53.126	26.558	1.00	32.97	A	C
ATOM	696	CB	TYR	A	211	25.782	51.691	26.439	1.00	33.26	A	C
ATOM	697	CG	TYR	A	211	24.709	50.628	26.361	1.00	32.75	A	C
ATOM	698	CD1	TYR	A	211	23.845	50.564	25.266	1.00	34.54	A	C
ATOM	699	CE1	TYR	A	211	22.802	49.649	25.223	1.00	35.34	A	C
ATOM	700	CD2	TYR	A	211	24.507	49.732	27.414	1.00	34.61	A	C
ATOM	701	CE2	TYR	A	211	23.461	48.807	27.385	1.00	35.43	A	C
ATOM	702	CZ	TYR	A	211	22.609	48.774	26.288	1.00	38.58	A	C
ATOM	703	OH	TYR	A	211	21.538	47.896	26.267	1.00	38.81	A	O
ATOM	704	C	TYR	A	211	24.260	53.213	27.735	1.00	33.39	A	C
ATOM	705	O	TYR	A	211	24.671	53.179	28.894	1.00	34.96	A	O
ATOM	706	N	ALA	A	212	22.972	53.352	27.425	1.00	33.87	A	N
ATOM	707	CA	ALA	A	212	21.920	53.438	28.441	1.00	35.11	A	C
ATOM	708	CB	ALA	A	212	20.919	54.559	28.080	1.00	34.05	A	C
ATOM	709	C	ALA	A	212	21.230	52.071	28.452	1.00	36.01	A	C
ATOM	710	O	ALA	A	212	20.408	51.757	27.578	1.00	36.24	A	O
ATOM	711	N	PRO	A	213	21.531	51.250	29.471	1.00	37.45	A	N
ATOM	712	CD	PRO	A	213	22.357	51.610	30.640	1.00	35.55	A	C
ATOM	713	CA	PRO	A	213	20.982	49.900	29.623	1.00	36.93	A	C
ATOM	714	CB	PRO	A	213	21.830	49.324	30.754	1.00	36.23	A	C
ATOM	715	CG	PRO	A	213	22.033	50.511	31.627	1.00	37.14	A	C
ATOM	716	C	PRO	A	213	19.493	49.694	29.857	1.00	37.75	A	C
ATOM	717	O	PRO	A	213	18.933	48.701	29.386	1.00	36.37	A	O
ATOM	718	N	LEU	A	214	18.837	50.612	30.560	1.00	36.70	A	N
ATOM	719	CA	LEU	A	214	17.418	50.415	30.846	1.00	37.91	A	C
ATOM	720	CB	LEU	A	214	17.104	50.906	32.266	1.00	36.60	A	C
ATOM	721	CG	LEU	A	214	17.399	49.897	33.394	1.00	37.61	A	C
ATOM	722	CD1	LEU	A	214	18.858	49.506	33.397	1.00	37.59	A	C
ATOM	723	CD2	LEU	A	214	17.028	50.497	34.736	1.00	36.22	A	C
ATOM	724	C	LEU	A	214	16.371	50.939	29.859	1.00	38.39	A	C
ATOM	725	O	LEU	A	214	15.182	50.954	30.173	1.00	38.54	A	O
ATOM	726	N	GLY	A	215	16.797	51.355	28.669	1.00	38.88	A	N
ATOM	727	CA	GLY	A	215	15.845	51.820	27.671	1.00	39.34	A	C
ATOM	728	C	GLY	A	215	15.322	53.244	27.782	1.00	37.48	A	C
ATOM	729	O	GLY	A	215	15.892	54.079	28.483	1.00	37.79	A	O
ATOM	730	N	THR	A	216	14.226	53.517	27.079	1.00	36.14	A	N
ATOM	731	CA	THR	A	216	13.642	54.862	27.066	1.00	36.67	A	C
ATOM	732	CB	THR	A	216	13.132	55.254	25.657	1.00	36.78	A	C
ATOM	733	OG1	THR	A	216	11.980	54.461	25.327	1.00	37.06	A	O
ATOM	734	CG2	THR	A	216	14.219	55.026	24.596	1.00	34.73	A	C
ATOM	735	C	THR	A	216	12.470	55.056	28.018	1.00	36.30	A	C
ATOM	736	O	THR	A	216	11.785	54.106	28.404	1.00	35.69	A	O
ATOM	737	N	VAL	A	217	12.254	56.311	28.391	1.00	38.14	A	N
ATOM	738	CA	VAL	A	217	11.147	56.686	29.258	1.00	38.24	A	C
ATOM	739	CB	VAL	A	217	11.180	58.209	29.559	1.00	38.38	A	C
ATOM	740	CG1	VAL	A	217	9.903	58.642	30.269	1.00	38.16	A	C
ATOM	741	CG2	VAL	A	217	12.394	58.532	30.418	1.00	34.69	A	C
ATOM	742	C	VAL	A	217	9.872	56.328	28.497	1.00	38.49	A	C
ATOM	743	O	VAL	A	217	8.865	55.949	29.087	1.00	38.84	A	O
ATOM	744	N	TYR	A	218	9.934	56.432	27.176	1.00	39.52	A	N
ATOM	745	CA	TYR	A	218	8.793	56.105	26.338	1.00	44.49	A	C
ATOM	746	CB	TYR	A	218	9.128	56.352	24.868	1.00	47.79	A	C
ATOM	747	CG	TYR	A	218	8.037	55.903	23.932	1.00	53.55	A	C
ATOM	748	CD1	TYR	A	218	8.292	54.963	22.934	1.00	55.54	A	C
ATOM	749	CE1	TYR	A	218	7.278	54.518	22.087	1.00	59.77	A	C
ATOM	750	CD2	TYR	A	218	6.738	56.394	24.060	1.00	57.06	A	C

ATOM	751	CE2	TYR	A	218	5.714	55.957	23.219	1.00	59.73	A	C
ATOM	752	CZ	TYR	A	218	5.993	55.018	22.235	1.00	61.61	A	C
ATOM	753	OH	TYR	A	218	4.986	54.575	21.402	1.00	65.83	A	O
ATOM	754	C	TYR	A	218	8.324	54.655	26.523	1.00	45.40	A	C
ATOM	755	O	TYR	A	218	7.131	54.409	26.740	1.00	44.19	A	O
ATOM	756	N	ARG	A	219	9.248	53.698	26.436	1.00	44.49	A	N
ATOM	757	CA	ARG	A	219	8.875	52.290	26.605	1.00	46.38	A	C
ATOM	758	CB	ARG	A	219	10.069	51.355	26.324	1.00	47.75	A	C
ATOM	759	CG	ARG	A	219	9.690	49.883	26.517	1.00	55.47	A	C
ATOM	760	CD	ARG	A	219	10.682	48.919	25.869	1.00	63.31	A	C
ATOM	761	NE	ARG	A	219	10.197	47.538	25.933	1.00	68.90	A	N
ATOM	762	CZ	ARG	A	219	10.723	46.518	25.260	1.00	70.39	A	C
ATOM	763	NH1	ARG	A	219	11.766	46.714	24.460	1.00	71.45	A	N
ATOM	764	NH2	ARG	A	219	10.199	45.301	25.382	1.00	70.62	A	N
ATOM	765	C	ARG	A	219	8.349	52.033	28.015	1.00	44.03	A	C
ATOM	766	O	ARG	A	219	7.381	51.297	28.202	1.00	41.33	A	O
ATOM	767	N	GLU	A	220	8.991	52.647	29.004	1.00	44.46	A	N
ATOM	768	CA	GLU	A	220	8.567	52.505	30.395	1.00	46.08	A	C
ATOM	769	CB	GLU	A	220	9.534	53.261	31.315	1.00	47.47	A	C
ATOM	770	CG	GLU	A	220	9.059	53.418	32.753	1.00	52.18	A	C
ATOM	771	CD	GLU	A	220	10.098	54.084	33.661	1.00	55.45	A	C
ATOM	772	OE1	GLU	A	220	10.628	55.158	33.296	1.00	55.13	A	O
ATOM	773	OE2	GLU	A	220	10.379	53.533	34.751	1.00	56.93	A	O
ATOM	774	C	GLU	A	220	7.144	53.050	30.550	1.00	45.87	A	C
ATOM	775	O	GLU	A	220	6.367	52.568	31.375	1.00	43.91	A	O
ATOM	776	N	LEU	A	221	6.801	54.045	29.737	1.00	44.52	A	N
ATOM	777	CA	LEU	A	221	5.473	54.649	29.789	1.00	45.19	A	C
ATOM	778	CB	LEU	A	221	5.483	55.989	29.036	1.00	45.91	A	C
ATOM	779	CG	LEU	A	221	4.363	57.008	29.278	1.00	47.69	A	C
ATOM	780	CD1	LEU	A	221	4.268	57.346	30.755	1.00	46.44	A	C
ATOM	781	CD2	LEU	A	221	4.646	58.270	28.470	1.00	47.40	A	C
ATOM	782	C	LEU	A	221	4.465	53.674	29.170	1.00	46.08	A	C
ATOM	783	O	LEU	A	221	3.320	53.580	29.617	1.00	44.50	A	O
ATOM	784	N	GLN	A	222	4.893	52.949	28.139	1.00	46.94	A	N
ATOM	785	CA	GLN	A	222	4.024	51.960	27.505	1.00	50.56	A	C
ATOM	786	CB	GLN	A	222	4.715	51.299	26.313	1.00	52.06	A	C
ATOM	787	CG	GLN	A	222	4.828	52.143	25.069	1.00	56.98	A	C
ATOM	788	CD	GLN	A	222	5.281	51.318	23.882	1.00	61.40	A	C
ATOM	789	OE1	GLN	A	222	6.287	50.607	23.958	1.00	64.80	A	O
ATOM	790	NE2	GLN	A	222	4.542	51.403	22.776	1.00	61.65	A	N
ATOM	791	C	GLN	A	222	3.701	50.872	28.528	1.00	50.28	A	C
ATOM	792	O	GLN	A	222	2.572	50.385	28.609	1.00	48.43	A	O
ATOM	793	N	LYS	A	223	4.718	50.502	29.301	1.00	51.04	A	N
ATOM	794	CA	LYS	A	223	4.604	49.475	30.332	1.00	52.24	A	C
ATOM	795	CB	LYS	A	223	5.992	49.146	30.895	1.00	53.80	A	C
ATOM	796	CG	LYS	A	223	6.680	47.951	30.261	1.00	57.08	A	C
ATOM	797	CD	LYS	A	223	6.939	48.120	28.773	1.00	59.58	A	C
ATOM	798	CE	LYS	A	223	7.506	46.821	28.187	1.00	62.45	A	C
ATOM	799	NZ	LYS	A	223	7.723	46.877	26.711	1.00	65.10	A	N
ATOM	800	C	LYS	A	223	3.680	49.855	31.488	1.00	51.07	A	C
ATOM	801	O	LYS	A	223	2.678	49.188	31.731	1.00	51.74	A	O
ATOM	802	N	LEU	A	224	4.024	50.927	32.195	1.00	49.30	A	N
ATOM	803	CA	LEU	A	224	3.250	51.382	33.347	1.00	47.99	A	C
ATOM	804	CB	LEU	A	224	4.153	52.201	34.272	1.00	45.38	A	C
ATOM	805	CG	LEU	A	224	5.509	51.562	34.588	1.00	45.90	A	C
ATOM	806	CD1	LEU	A	224	6.327	52.477	35.475	1.00	43.89	A	C
ATOM	807	CD2	LEU	A	224	5.291	50.228	35.263	1.00	47.72	A	C
ATOM	808	C	LEU	A	224	1.979	52.183	33.067	1.00	47.57	A	C
ATOM	809	O	LEU	A	224	1.198	52.417	33.986	1.00	48.98	A	O
ATOM	810	N	SER	A	225	1.770	52.596	31.818	1.00	47.50	A	N
ATOM	811	CA	SER	A	225	0.602	53.397	31.432	1.00	46.59	A	C
ATOM	812	CB	SER	A	225	-0.682	52.840	32.053	1.00	48.00	A	C
ATOM	813	OG	SER	A	225	-1.018	51.593	31.477	1.00	51.00	A	O
ATOM	814	C	SER	A	225	0.790	54.850	31.862	1.00	46.78	A	C
ATOM	815	O	SER	A	225	0.652	55.771	31.056	1.00	46.17	A	O
ATOM	816	N	LYS	A	226	1.113	55.043	33.136	1.00	45.76	A	N
ATOM	817	CA	LYS	A	226	1.349	56.371	33.690	1.00	45.69	A	C
ATOM	818	CB	LYS	A	226	0.019	57.049	34.025	1.00	48.92	A	C
ATOM	819	CG	LYS	A	226	-0.896	56.251	34.937	1.00	50.24	A	C
ATOM	820	CD	LYS	A	226	-2.286	56.871	34.944	1.00	55.99	A	C
ATOM	821	CE	LYS	A	226	-3.213	56.217	35.960	1.00	56.96	A	C
ATOM	822	NZ	LYS	A	226	-4.577	56.820	35.924	1.00	58.58	A	N

ATOM	823	C	LYS	A	226	2.211	56.235	34.935	1.00	43.87	A	C
ATOM	824	O	LYS	A	226	2.219	55.180	35.563	1.00	43.31	A	O
ATOM	825	N	PHE	A	227	2.945	57.291	35.280	1.00	42.51	A	N
ATOM	826	CA	PHE	A	227	3.822	57.271	36.446	1.00	41.32	A	C
ATOM	827	CB	PHE	A	227	5.136	58.018	36.163	1.00	38.84	A	C
ATOM	828	CG	PHE	A	227	5.901	57.493	34.969	1.00	38.42	A	C
ATOM	829	CD1	PHE	A	227	5.793	56.155	34.574	1.00	34.24	A	C
ATOM	830	CD2	PHE	A	227	6.741	58.338	34.242	1.00	37.52	A	C
ATOM	831	CE1	PHE	A	227	6.506	55.673	33.477	1.00	33.25	A	C
ATOM	832	CE2	PHE	A	227	7.460	57.859	33.139	1.00	37.09	A	C
ATOM	833	CZ	PHE	A	227	7.340	56.525	32.760	1.00	31.91	A	C
ATOM	834	C	PHE	A	227	3.168	57.888	37.669	1.00	44.70	A	C
ATOM	835	O	PHE	A	227	2.199	58.644	37.554	1.00	45.27	A	O
ATOM	836	N	ASP	A	228	3.708	57.572	38.844	1.00	44.53	A	N
ATOM	837	CA	ASP	A	228	3.170	58.115	40.078	1.00	45.73	A	C
ATOM	838	CB	ASP	A	228	3.357	57.121	41.234	1.00	47.95	A	C
ATOM	839	CG	ASP	A	228	4.797	57.012	41.696	1.00	50.80	A	C
ATOM	840	OD1	ASP	A	228	5.711	57.200	40.871	1.00	55.59	A	O
ATOM	841	OD2	ASP	A	228	5.016	56.718	42.889	1.00	53.57	A	O
ATOM	842	O	ASP	A	228	3.873	59.435	40.363	1.00	44.84	A	C
ATOM	843	O	ASP	A	228	4.805	59.815	39.655	1.00	42.73	A	O
ATOM	844	N	GLU	A	229	3.419	60.130	41.400	1.00	44.06	A	N
ATOM	845	CA	GLU	A	229	3.986	61.419	41.769	1.00	44.15	A	C
ATOM	846	CB	GLU	A	229	3.176	62.046	42.914	1.00	46.01	A	C
ATOM	847	CG	GLU	A	229	1.732	62.358	42.554	1.00	49.15	A	C
ATOM	848	CD	GLU	A	229	1.149	63.475	43.398	1.00	53.31	A	C
ATOM	849	OE1	GLU	A	229	1.055	63.311	44.633	1.00	54.33	A	O
ATOM	850	OE2	GLU	A	229	0.785	64.525	42.823	1.00	57.15	A	O
ATOM	851	C	GLU	A	229	5.459	61.412	42.146	1.00	42.45	A	C
ATOM	852	O	GLU	A	229	6.189	62.330	41.778	1.00	42.84	A	O
ATOM	853	N	GLN	A	230	5.904	60.399	42.889	1.00	42.42	A	N
ATOM	854	CA	GLN	A	230	7.309	60.355	43.291	1.00	40.75	A	C
ATOM	855	CB	GLN	A	230	7.583	59.227	44.302	1.00	43.22	A	C
ATOM	856	CG	GLN	A	230	9.034	59.251	44.825	1.00	46.84	A	C
ATOM	857	CD	GLN	A	230	9.369	58.120	45.789	1.00	51.94	A	C
ATOM	858	OE1	GLN	A	230	9.463	56.955	45.397	1.00	55.25	A	O
ATOM	859	NE2	GLN	A	230	9.558	58.464	47.059	1.00	53.28	A	N
ATOM	860	C	GLN	A	230	8.233	60.171	42.095	1.00	38.22	A	C
ATOM	861	O	GLN	A	230	9.274	60.816	42.014	1.00	37.20	A	O
ATOM	862	N	ARG	A	231	7.851	59.286	41.176	1.00	36.78	A	N
ATOM	863	CA	ARG	A	231	8.663	59.017	39.997	1.00	39.10	A	C
ATOM	864	CB	ARG	A	231	8.186	57.749	39.284	1.00	37.47	A	C
ATOM	865	CG	ARG	A	231	9.122	57.330	38.158	1.00	39.31	A	C
ATOM	866	CD	ARG	A	231	8.420	56.555	37.057	1.00	41.69	A	C
ATOM	867	NE	ARG	A	231	8.185	55.146	37.380	1.00	47.47	A	N
ATOM	868	CZ	ARG	A	231	9.134	54.213	37.466	1.00	51.32	A	C
ATOM	869	NH1	ARG	A	231	8.799	52.963	37.761	1.00	52.36	A	N
ATOM	870	NH2	ARG	A	231	10.416	54.515	37.266	1.00	48.44	A	N
ATOM	871	C	ARG	A	231	8.635	60.192	39.013	1.00	38.58	A	C
ATOM	872	O	ARG	A	231	9.640	60.497	38.381	1.00	37.91	A	O
ATOM	873	N	THR	A	232	7.477	60.836	38.878	1.00	39.25	A	N
ATOM	874	CA	THR	A	232	7.336	61.980	37.980	1.00	36.38	A	C
ATOM	875	CB	THR	A	232	5.866	62.434	37.888	1.00	35.78	A	C
ATOM	876	OG1	THR	A	232	5.077	61.377	37.327	1.00	33.52	A	O
ATOM	877	CG2	THR	A	232	5.740	63.684	37.014	1.00	33.99	A	C
ATOM	878	C	THR	A	232	8.176	63.157	38.475	1.00	37.94	A	C
ATOM	879	O	THR	A	232	8.906	63.780	37.708	1.00	39.65	A	O
ATOM	880	N	ALA	A	233	8.085	63.445	39.769	1.00	38.61	A	N
ATOM	881	CA	ALA	A	233	8.820	64.556	40.364	1.00	39.65	A	C
ATOM	882	CB	ALA	A	233	8.374	64.757	41.810	1.00	39.86	A	C
ATOM	883	C	ALA	A	233	10.333	64.359	40.304	1.00	39.68	A	C
ATOM	884	O	ALA	A	233	11.085	65.318	40.118	1.00	39.18	A	O
ATOM	885	N	THR	A	234	10.783	63.120	40.474	1.00	39.91	A	N
ATOM	886	CA	THR	A	234	12.214	62.838	40.421	1.00	39.28	A	C
ATOM	887	CB	THR	A	234	12.517	61.360	40.828	1.00	39.65	A	C
ATOM	888	OG1	THR	A	234	11.901	61.073	42.086	1.00	36.77	A	O
ATOM	889	CG2	THR	A	234	14.006	61.131	40.978	1.00	39.65	A	C
ATOM	890	C	THR	A	234	12.687	63.096	38.991	1.00	38.18	A	C
ATOM	891	O	THR	A	234	13.685	63.780	38.775	1.00	41.05	A	O
ATOM	892	N	TYR	A	235	11.953	62.559	38.015	1.00	39.28	A	N
ATOM	893	CA	TYR	A	235	12.300	62.737	36.602	1.00	38.40	A	C
ATOM	894	CB	TYR	A	235	11.293	62.018	35.700	1.00	38.30	A	C

ATOM	895	CG	TYR	A	235	11.446	60.517	35.606	1.00	40.28	A	C
ATOM	896	CD1	TYR	A	235	12.516	59.853	36.209	1.00	41.54	A	C
ATOM	897	CE1	TYR	A	235	12.668	58.463	36.079	1.00	42.34	A	C
ATOM	898	CD2	TYR	A	235	10.532	59.761	34.878	1.00	39.41	A	C
ATOM	899	CE2	TYR	A	235	10.670	58.387	34.746	1.00	40.62	A	C
ATOM	900	CZ	TYR	A	235	11.737	57.738	35.344	1.00	42.31	A	C
ATOM	901	OH	TYR	A	235	11.866	56.370	35.191	1.00	40.25	A	O
ATOM	902	C	TYR	A	235	12.358	64.213	36.207	1.00	38.07	A	C
ATOM	903	O	TYR	A	235	13.259	64.629	35.482	1.00	36.19	A	O
ATOM	904	N	ILE	A	236	11.392	65.002	36.678	1.00	39.25	A	N
ATOM	905	CA	ILE	A	236	11.370	66.434	36.374	1.00	37.44	A	C
ATOM	906	CB	ILE	A	236	10.064	67.102	36.872	1.00	37.12	A	C
ATOM	907	CG2	ILE	A	236	10.170	68.627	36.741	1.00	34.15	A	C
ATOM	908	CG1	ILE	A	236	8.878	66.554	36.072	1.00	35.02	A	C
ATOM	909	CD1	ILE	A	236	8.997	66.750	34.561	1.00	36.77	A	C
ATOM	910	C	ILE	A	236	12.574	67.115	37.012	1.00	37.57	A	C
ATOM	911	O	ILE	A	236	13.172	68.022	36.426	1.00	40.12	A	O
ATOM	912	N	THR	A	237	12.941	66.668	38.209	1.00	36.62	A	N
ATOM	913	CA	THR	A	237	14.114	67.215	38.891	1.00	36.77	A	C
ATOM	914	CB	THR	A	237	14.285	66.590	40.310	1.00	36.70	A	C
ATOM	915	OG1	THR	A	237	13.174	66.970	41.134	1.00	39.88	A	O
ATOM	916	CG2	THR	A	237	15.592	67.072	40.970	1.00	33.73	A	C
ATOM	917	C	THR	A	237	15.393	66.931	38.084	1.00	36.40	A	C
ATOM	918	O	THR	A	237	16.244	67.808	37.917	1.00	34.72	A	O
ATOM	919	N	GLU	A	238	15.531	65.703	37.589	1.00	35.89	A	N
ATOM	920	CA	GLU	A	238	16.724	65.343	36.826	1.00	36.31	A	C
ATOM	921	CB	GLU	A	238	16.743	63.831	36.584	1.00	37.43	A	C
ATOM	922	CG	GLU	A	238	16.699	63.014	37.882	1.00	39.75	A	C
ATOM	923	CD	GLU	A	238	16.579	61.516	37.652	1.00	42.37	A	C
ATOM	924	OE1	GLU	A	238	16.240	61.106	36.526	1.00	46.02	A	O
ATOM	925	OE2	GLU	A	238	16.804	60.739	38.605	1.00	44.16	A	O
ATOM	926	C	GLU	A	238	16.792	66.124	35.508	1.00	36.97	A	C
ATOM	927	O	GLU	A	238	17.875	66.515	35.068	1.00	38.41	A	O
ATOM	928	N	LEU	A	239	15.634	66.371	34.898	1.00	37.50	A	N
ATOM	929	CA	LEU	A	239	15.551	67.133	33.646	1.00	36.81	A	C
ATOM	930	CB	LEU	A	239	14.142	67.020	33.063	1.00	35.68	A	C
ATOM	931	CG	LEU	A	239	13.804	65.710	32.362	1.00	39.17	A	C
ATOM	932	CD1	LEU	A	239	12.292	65.600	32.137	1.00	37.66	A	C
ATOM	933	CD2	LEU	A	239	14.575	65.663	31.041	1.00	37.84	A	C
ATOM	934	C	LEU	A	239	15.875	68.613	33.852	1.00	35.88	A	C
ATOM	935	O	LEU	A	239	16.629	69.219	33.085	1.00	34.18	A	O
ATOM	936	N	ALA	A	240	15.294	69.198	34.892	1.00	37.08	A	N
ATOM	937	CA	ALA	A	240	15.526	70.613	35.171	1.00	37.40	A	C
ATOM	938	CB	ALA	A	240	14.677	71.059	36.375	1.00	35.91	A	C
ATOM	939	C	ALA	A	240	17.011	70.863	35.426	1.00	37.09	A	C
ATOM	940	O	ALA	A	240	17.558	71.896	35.024	1.00	35.00	A	O
ATOM	941	N	ASN	A	241	17.661	69.909	36.092	1.00	38.15	A	N
ATOM	942	CA	ASN	A	241	19.092	70.010	36.387	1.00	37.31	A	C
ATOM	943	CB	ASN	A	241	19.562	68.864	37.294	1.00	39.88	A	C
ATOM	944	CG	ASN	A	241	19.152	69.053	38.733	1.00	44.02	A	C
ATOM	945	OD1	ASN	A	241	19.346	70.125	39.308	1.00	47.57	A	O
ATOM	946	ND2	ASN	A	241	18.588	68.006	39.331	1.00	46.92	A	N
ATOM	947	C	ASN	A	241	19.920	69.962	35.119	1.00	36.22	A	C
ATOM	948	O	ASN	A	241	20.871	70.724	34.975	1.00	36.76	A	O
ATOM	949	N	ALA	A	242	19.585	69.041	34.217	1.00	33.89	A	N
ATOM	950	CA	ALA	A	242	20.328	68.916	32.963	1.00	34.20	A	C
ATOM	951	CB	ALA	A	242	19.869	67.669	32.178	1.00	31.75	A	C
ATOM	952	C	ALA	A	242	20.121	70.173	32.125	1.00	33.01	A	C
ATOM	953	O	ALA	A	242	21.073	70.719	31.574	1.00	33.65	A	O
ATOM	954	N	LEU	A	243	18.875	70.630	32.043	1.00	33.50	A	N
ATOM	955	CA	LEU	A	243	18.554	71.830	31.279	1.00	36.89	A	C
ATOM	956	CB	LEU	A	243	17.031	71.999	31.183	1.00	34.36	A	C
ATOM	957	CG	LEU	A	243	16.331	70.888	30.385	1.00	35.75	A	C
ATOM	958	CD1	LEU	A	243	14.827	71.111	30.357	1.00	36.43	A	C
ATOM	959	CD2	LEU	A	243	16.884	70.867	28.965	1.00	34.93	A	C
ATOM	960	C	LEU	A	243	19.218	73.098	31.848	1.00	38.16	A	C
ATOM	961	O	LEU	A	243	19.666	73.956	31.083	1.00	38.31	A	O
ATOM	962	N	SER	A	244	19.296	73.219	33.175	1.00	39.80	A	N
ATOM	963	CA	SER	A	244	19.945	74.391	33.778	1.00	40.44	A	C
ATOM	964	CB	SER	A	244	19.861	74.357	35.308	1.00	43.11	A	C
ATOM	965	OG	SER	A	244	18.521	74.198	35.743	1.00	47.97	A	O
ATOM	966	C	SER	A	244	21.411	74.365	33.369	1.00	40.05	A	C

ATOM	967	O	SER	A	244	22.001	75.396	33.021	1.00	40.00	A	O
ATOM	968	N	TYR	A	245	22.005	73.177	33.413	1.00	37.27	A	N
ATOM	969	CA	TYR	A	245	23.400	73.053	33.021	1.00	35.82	A	C
ATOM	970	CB	TYR	A	245	23.897	71.622	33.252	1.00	35.21	A	C
ATOM	971	CG	TYR	A	245	25.202	71.317	32.555	1.00	37.03	A	C
ATOM	972	CD1	TYR	A	245	25.215	70.770	31.274	1.00	36.51	A	C
ATOM	973	CE1	TYR	A	245	26.410	70.511	30.613	1.00	40.47	A	C
ATOM	974	CD2	TYR	A	245	26.426	71.603	33.163	1.00	38.38	A	C
ATOM	975	CE2	TYR	A	245	27.630	71.350	32.507	1.00	41.25	A	C
ATOM	976	CZ	TYR	A	245	27.612	70.800	31.231	1.00	40.43	A	C
ATOM	977	OH	TYR	A	245	28.788	70.527	30.576	1.00	43.84	A	O
ATOM	978	C	TYR	A	245	23.561	73.448	31.550	1.00	35.32	A	C
ATOM	979	O	TYR	A	245	24.479	74.176	31.200	1.00	35.27	A	O
ATOM	980	N	CYS	A	246	22.661	72.971	30.694	1.00	36.27	A	N
ATOM	981	CA	CYS	A	246	22.721	73.295	29.267	1.00	38.83	A	C
ATOM	982	CB	CYS	A	246	21.609	72.568	28.498	1.00	38.59	A	C
ATOM	983	SG	CYS	A	246	21.897	70.797	28.263	1.00	44.30	A	S
ATOM	984	C	CYS	A	246	22.606	74.802	29.031	1.00	39.39	A	C
ATOM	985	O	CYS	A	246	23.322	75.358	28.200	1.00	37.11	A	O
ATOM	986	N	HIS	A	247	21.704	75.461	29.756	1.00	40.65	A	N
ATOM	987	CA	HIS	A	247	21.542	76.903	29.603	1.00	43.91	A	C
ATOM	988	CB	HIS	A	247	20.403	77.414	30.493	1.00	44.23	A	C
ATOM	989	CG	HIS	A	247	19.038	77.074	29.978	1.00	45.59	A	C
ATOM	990	CD2	HIS	A	247	18.645	76.412	28.862	1.00	45.56	A	C
ATOM	991	ND1	HIS	A	247	17.881	77.447	30.628	1.00	45.85	A	N
ATOM	992	CE1	HIS	A	247	16.834	77.033	29.937	1.00	46.13	A	C
ATOM	993	NE2	HIS	A	247	17.270	76.402	28.861	1.00	48.11	A	N
ATOM	994	C	HIS	A	247	22.840	77.642	29.931	1.00	46.24	A	C
ATOM	995	O	HIS	A	247	23.223	78.581	29.231	1.00	46.66	A	O
ATOM	996	N	SER	A	248	23.527	77.213	30.985	1.00	46.80	A	N
ATOM	997	CA	SER	A	248	24.780	77.858	31.359	1.00	47.62	A	C
ATOM	998	CB	SER	A	248	25.344	77.247	32.653	1.00	46.92	A	C
ATOM	999	OG	SER	A	248	25.872	75.950	32.432	1.00	48.53	A	O
ATOM	1000	C	SER	A	248	25.799	77.716	30.223	1.00	47.38	A	C
ATOM	1001	O	SER	A	248	26.774	78.469	30.152	1.00	48.22	A	O
ATOM	1002	N	LYS	A	249	25.566	76.761	29.328	1.00	45.39	A	N
ATOM	1003	CA	LYS	A	249	26.473	76.541	28.209	1.00	46.59	A	C
ATOM	1004	CB	LYS	A	249	26.731	75.047	28.021	1.00	44.79	A	C
ATOM	1005	CG	LYS	A	249	27.091	74.323	29.300	1.00	49.43	A	C
ATOM	1006	CD	LYS	A	249	28.337	74.902	29.951	1.00	52.06	A	C
ATOM	1007	CE	LYS	A	249	29.587	74.520	29.183	1.00	56.23	A	C
ATOM	1008	NZ	LYS	A	249	29.806	73.040	29.150	1.00	58.63	A	N
ATOM	1009	C	LYS	A	249	25.909	77.131	26.919	1.00	48.59	A	C
ATOM	1010	O	LYS	A	249	26.490	76.966	25.847	1.00	47.53	A	O
ATOM	1011	N	ARG	A	250	24.769	77.808	27.032	1.00	51.35	A	N
ATOM	1012	CA	ARG	A	250	24.117	78.434	25.884	1.00	55.46	A	C
ATOM	1013	CB	ARG	A	250	25.079	79.425	25.204	1.00	58.41	A	C
ATOM	1014	CG	ARG	A	250	25.543	80.543	26.151	1.00	64.68	A	C
ATOM	1015	CD	ARG	A	250	26.350	81.658	25.464	1.00	69.77	A	C
ATOM	1016	NE	ARG	A	250	27.615	81.204	24.886	1.00	72.33	A	N
ATOM	1017	CZ	ARG	A	250	28.584	82.020	24.473	1.00	74.30	A	C
ATOM	1018	NH1	ARG	A	250	28.439	83.338	24.574	1.00	73.90	A	N
ATOM	1019	NH2	ARG	A	250	29.699	81.520	23.951	1.00	74.27	A	N
ATOM	1020	C	ARG	A	250	23.606	77.401	24.884	1.00	54.89	A	C
ATOM	1021	O	ARG	A	250	23.589	77.635	23.671	1.00	55.10	A	O
ATOM	1022	N	VAL	A	251	23.196	76.252	25.413	1.00	53.65	A	N
ATOM	1023	CA	VAL	A	251	22.658	75.169	24.605	1.00	51.49	A	C
ATOM	1024	CB	VAL	A	251	23.343	73.815	24.924	1.00	51.47	A	C
ATOM	1025	CG1	VAL	A	251	22.550	72.664	24.310	1.00	47.16	A	C
ATOM	1026	CG2	VAL	A	251	24.761	73.809	24.378	1.00	51.44	A	C
ATOM	1027	C	VAL	A	251	21.175	75.052	24.927	1.00	52.04	A	C
ATOM	1028	O	VAL	A	251	20.793	74.885	26.090	1.00	50.43	A	O
ATOM	1029	N	ILE	A	252	20.348	75.158	23.894	1.00	51.36	A	N
ATOM	1030	CA	ILE	A	252	18.908	75.050	24.049	1.00	52.79	A	C
ATOM	1031	CB	ILE	A	252	18.205	76.372	23.690	1.00	54.02	A	C
ATOM	1032	CG2	ILE	A	252	16.696	76.214	23.823	1.00	54.66	A	C
ATOM	1033	CG1	ILE	A	252	18.709	77.490	24.611	1.00	54.46	A	C
ATOM	1034	CD1	ILE	A	252	18.176	78.868	24.259	1.00	55.53	A	C
ATOM	1035	C	ILE	A	252	18.434	73.950	23.113	1.00	53.85	A	C
ATOM	1036	O	ILE	A	252	18.911	73.841	21.984	1.00	54.35	A	O
ATOM	1037	N	HIS	A	253	17.515	73.124	23.602	1.00	54.36	A	N
ATOM	1038	CA	HIS	A	253	16.964	72.021	22.824	1.00	54.56	A	C

ATOM	1039	CB	HIS	A	253	16.590	70.840	23.736	1.00	52.75	A	C
ATOM	1040	CG	HIS	A	253	17.757	70.216	24.438	1.00	52.00	A	C
ATOM	1041	CD2	HIS	A	253	18.281	68.970	24.359	1.00	52.22	A	C
ATOM	1042	ND1	HIS	A	253	18.546	70.907	25.334	1.00	50.80	A	N
ATOM	1043	CE1	HIS	A	253	19.509	70.115	25.771	1.00	50.65	A	C
ATOM	1044	NE2	HIS	A	253	19.372	68.934	25.195	1.00	52.67	A	N
ATOM	1045	C	HIS	A	253	15.715	72.509	22.115	1.00	55.98	A	C
ATOM	1046	O	HIS	A	253	15.189	73.579	22.423	1.00	53.17	A	O
ATOM	1047	N	ARG	A	254	15.247	71.716	21.161	1.00	59.64	A	N
ATOM	1048	CA	ARG	A	254	14.046	72.048	20.412	1.00	63.55	A	C
ATOM	1049	CB	ARG	A	254	14.391	72.384	18.956	1.00	67.04	A	C
ATOM	1050	CG	ARG	A	254	15.314	73.592	18.803	1.00	72.33	A	C
ATOM	1051	CD	ARG	A	254	15.366	74.081	17.357	1.00	76.66	A	C
ATOM	1052	NE	ARG	A	254	16.348	75.148	17.165	1.00	79.26	A	N
ATOM	1053	CZ	ARG	A	254	16.488	75.840	16.037	1.00	80.83	A	C
ATOM	1054	NH1	ARG	A	254	15.706	75.581	14.997	1.00	81.15	A	N
ATOM	1055	NH2	ARG	A	254	17.413	76.787	15.944	1.00	81.58	A	N
ATOM	1056	C	ARG	A	254	13.133	70.831	20.476	1.00	63.27	A	C
ATOM	1057	O	ARG	A	254	13.176	69.967	19.607	1.00	65.67	A	O
ATOM	1058	N	ASP	A	255	12.327	70.776	21.531	1.00	60.76	A	N
ATOM	1059	CA	ASP	A	255	11.391	69.686	21.786	1.00	59.10	A	C
ATOM	1060	CB	ASP	A	255	10.512	69.404	20.549	1.00	59.56	A	C
ATOM	1061	CG	ASP	A	255	11.108	68.366	19.606	1.00	60.20	A	C
ATOM	1062	OD1	ASP	A	255	11.300	67.208	20.026	1.00	62.58	A	O
ATOM	1063	OD2	ASP	A	255	11.372	68.702	18.433	1.00	60.34	A	O
ATOM	1064	C	ASP	A	255	12.099	68.411	22.256	1.00	57.58	A	C
ATOM	1065	O	ASP	A	255	13.017	67.901	21.596	1.00	55.18	A	O
ATOM	1066	N	ILE	A	256	11.698	67.920	23.426	1.00	54.14	A	N
ATOM	1067	CA	ILE	A	256	12.285	66.695	23.948	1.00	52.47	A	C
ATOM	1068	CB	ILE	A	256	13.115	66.949	25.237	1.00	54.35	A	C
ATOM	1069	CG2	ILE	A	256	13.581	68.397	25.271	1.00	54.91	A	C
ATOM	1070	CG1	ILE	A	256	12.298	66.652	26.487	1.00	56.23	A	C
ATOM	1071	CD1	ILE	A	256	13.151	66.501	27.717	1.00	58.73	A	C
ATOM	1072	C	ILE	A	256	11.150	65.705	24.193	1.00	48.66	A	C
ATOM	1073	O	ILE	A	256	10.242	65.957	24.989	1.00	48.97	A	O
ATOM	1074	N	LYS	A	257	11.190	64.598	23.461	1.00	44.04	A	N
ATOM	1075	CA	LYS	A	257	10.164	63.569	23.551	1.00	42.42	A	C
ATOM	1076	CB	LYS	A	257	9.837	63.053	22.146	1.00	42.94	A	C
ATOM	1077	CG	LYS	A	257	9.671	64.158	21.119	1.00	47.60	A	C
ATOM	1078	CD	LYS	A	257	8.714	63.758	20.008	1.00	50.15	A	C
ATOM	1079	CE	LYS	A	257	9.278	62.672	19.115	1.00	54.00	A	C
ATOM	1080	NZ	LYS	A	257	8.244	62.166	18.147	1.00	55.95	A	N
ATOM	1081	C	LYS	A	257	10.575	62.395	24.446	1.00	40.38	A	C
ATOM	1082	O	LYS	A	257	11.761	62.170	24.688	1.00	40.25	A	O
ATOM	1083	N	PRO	A	258	9.592	61.631	24.944	1.00	38.26	A	N
ATOM	1084	CD	PRO	A	258	8.141	61.822	24.769	1.00	35.77	A	C
ATOM	1085	CA	PRO	A	258	9.866	60.479	25.809	1.00	39.42	A	C
ATOM	1086	CB	PRO	A	258	8.478	59.868	26.026	1.00	38.99	A	C
ATOM	1087	CG	PRO	A	258	7.571	61.051	25.941	1.00	38.85	A	C
ATOM	1088	C	PRO	A	258	10.838	59.483	25.173	1.00	38.24	A	C
ATOM	1089	O	PRO	A	258	11.621	58.855	25.876	1.00	37.93	A	O
ATOM	1090	N	GLU	A	259	10.795	59.352	23.848	1.00	39.21	A	N
ATOM	1091	CA	GLU	A	259	11.682	58.421	23.142	1.00	39.84	A	C
ATOM	1092	CB	GLU	A	259	11.188	58.155	21.716	1.00	40.55	A	C
ATOM	1093	CG	GLU	A	259	9.688	58.072	21.594	1.00	48.83	A	C
ATOM	1094	CD	GLU	A	259	9.081	59.411	21.225	1.00	50.31	A	C
ATOM	1095	OE1	GLU	A	259	7.919	59.679	21.604	1.00	51.19	A	O
ATOM	1096	OE2	GLU	A	259	9.776	60.190	20.536	1.00	54.44	A	O
ATOM	1097	C	GLU	A	259	13.121	58.909	23.070	1.00	38.93	A	C
ATOM	1098	O	GLU	A	259	14.011	58.149	22.694	1.00	36.58	A	O
ATOM	1099	N	ASN	A	260	13.347	60.176	23.413	1.00	38.55	A	N
ATOM	1100	CA	ASN	A	260	14.690	60.746	23.391	1.00	37.69	A	C
ATOM	1101	CB	ASN	A	260	14.694	62.115	22.702	1.00	42.07	A	C
ATOM	1102	CG	ASN	A	260	13.986	62.096	21.362	1.00	45.98	A	C
ATOM	1103	OD1	ASN	A	260	14.267	61.258	20.507	1.00	50.60	A	O
ATOM	1104	ND2	ASN	A	260	13.062	63.032	21.171	1.00	50.14	A	N
ATOM	1105	C	ASN	A	260	15.222	60.883	24.818	1.00	35.15	A	C
ATOM	1106	O	ASN	A	260	16.206	61.578	25.071	1.00	33.57	A	O
ATOM	1107	N	LEU	A	261	14.548	60.236	25.754	1.00	32.79	A	N
ATOM	1108	CA	LEU	A	261	14.995	60.242	27.146	1.00	35.15	A	C
ATOM	1109	CB	LEU	A	261	13.875	60.737	28.075	1.00	30.11	A	C
ATOM	1110	CG	LEU	A	261	13.410	62.179	27.822	1.00	29.12	A	C

ATOM	1111	CD1	LEU	A	261	12.459	62.616	28.925	1.00	21.95	A	C
ATOM	1112	CD2	LEU	A	261	14.624	63.110	27.765	1.00	29.74	A	C
ATOM	1113	C	LEU	A	261	15.366	58.785	27.462	1.00	35.15	A	C
ATOM	1114	O	LEU	A	261	14.499	57.911	27.498	1.00	34.65	A	O
ATOM	1115	N	LEU	A	262	16.656	58.528	27.657	1.00	35.80	A	N
ATOM	1116	CA	LEU	A	262	17.140	57.180	27.934	1.00	36.00	A	C
ATOM	1117	CB	LEU	A	262	18.439	56.923	27.167	1.00	36.54	A	C
ATOM	1118	CG	LEU	A	262	18.311	56.713	25.654	1.00	39.58	A	C
ATOM	1119	CD1	LEU	A	262	19.676	56.811	25.001	1.00	37.56	A	C
ATOM	1120	CD2	LEU	A	262	17.678	55.352	25.377	1.00	41.77	A	C
ATOM	1121	C	LEU	A	262	17.355	56.958	29.421	1.00	36.91	A	C
ATOM	1122	O	LEU	A	262	17.428	57.915	30.189	1.00	38.50	A	O
ATOM	1123	N	LEU	A	263	17.467	55.694	29.828	1.00	36.14	A	N
ATOM	1124	CA	LEU	A	263	17.640	55.364	31.246	1.00	35.96	A	C
ATOM	1125	CB	LEU	A	263	16.472	54.488	31.709	1.00	37.11	A	C
ATOM	1126	CG	LEU	A	263	15.116	55.210	31.748	1.00	36.12	A	C
ATOM	1127	CD1	LEU	A	263	14.003	54.231	32.073	1.00	36.15	A	C
ATOM	1128	CD2	LEU	A	263	15.168	56.321	32.782	1.00	32.38	A	C
ATOM	1129	C	LEU	A	263	18.965	54.690	31.584	1.00	36.75	A	C
ATOM	1130	O	LEU	A	263	19.305	53.648	31.022	1.00	35.94	A	O
ATOM	1131	N	GLY	A	264	19.700	55.301	32.512	1.00	36.23	A	N
ATOM	1132	CA	GLY	A	264	20.990	54.788	32.933	1.00	38.00	A	C
ATOM	1133	C	GLY	A	264	20.941	53.534	33.796	1.00	38.80	A	C
ATOM	1134	O	GLY	A	264	19.864	53.026	34.113	1.00	36.95	A	O
ATOM	1135	N	SER	A	265	22.122	53.060	34.193	1.00	39.31	A	N
ATOM	1136	CA	SER	A	265	22.271	51.844	34.999	1.00	40.86	A	C
ATOM	1137	CB	SER	A	265	23.758	51.555	35.232	1.00	40.25	A	C
ATOM	1138	OG	SER	A	265	23.942	50.288	35.847	1.00	45.33	A	O
ATOM	1139	C	SER	A	265	21.544	51.876	36.337	1.00	41.82	A	C
ATOM	1140	O	SER	A	265	21.030	50.852	36.800	1.00	43.16	A	O
ATOM	1141	N	ALA	A	266	21.506	53.048	36.962	1.00	43.56	A	N
ATOM	1142	CA	ALA	A	266	20.833	53.213	38.248	1.00	43.39	A	C
ATOM	1143	CB	ALA	A	266	21.603	54.213	39.126	1.00	41.16	A	C
ATOM	1144	C	ALA	A	266	19.402	53.701	38.037	1.00	42.96	A	C
ATOM	1145	O	ALA	A	266	18.709	54.053	38.987	1.00	44.36	A	O
ATOM	1146	N	GLY	A	267	18.960	53.722	36.787	1.00	43.26	A	N
ATOM	1147	CA	GLY	A	267	17.613	54.176	36.510	1.00	43.62	A	C
ATOM	1148	C	GLY	A	267	17.464	55.678	36.307	1.00	43.28	A	C
ATOM	1149	O	GLY	A	267	16.346	56.156	36.114	1.00	46.43	A	O
ATOM	1150	N	GLU	A	268	18.557	56.433	36.350	1.00	42.29	A	N
ATOM	1151	CA	GLU	A	268	18.456	57.881	36.147	1.00	42.87	A	C
ATOM	1152	CB	GLU	A	268	19.725	58.627	36.592	1.00	44.50	A	C
ATOM	1153	CG	GLU	A	268	20.796	57.769	37.220	1.00	50.35	A	C
ATOM	1154	CD	GLU	A	268	21.520	56.919	36.204	1.00	49.75	A	C
ATOM	1155	OE1	GLU	A	268	22.583	57.358	35.701	1.00	49.51	A	O
ATOM	1156	OE2	GLU	A	268	21.012	55.817	35.904	1.00	48.21	A	O
ATOM	1157	C	GLU	A	268	18.175	58.231	34.689	1.00	41.51	A	C
ATOM	1158	O	GLU	A	268	18.505	57.484	33.764	1.00	39.67	A	O
ATOM	1159	N	LEU	A	269	17.563	59.390	34.502	1.00	39.23	A	N
ATOM	1160	CA	LEU	A	269	17.206	59.881	33.185	1.00	38.66	A	C
ATOM	1161	CB	LEU	A	269	16.091	60.912	33.371	1.00	37.44	A	C
ATOM	1162	CG	LEU	A	269	15.367	61.562	32.205	1.00	38.26	A	C
ATOM	1163	CD1	LEU	A	269	13.995	62.029	32.680	1.00	32.98	A	C
ATOM	1164	CD2	LEU	A	269	16.203	62.718	31.665	1.00	40.16	A	C
ATOM	1165	C	LEU	A	269	18.418	60.480	32.447	1.00	36.13	A	C
ATOM	1166	O	LEU	A	269	19.255	61.153	33.050	1.00	34.63	A	O
ATOM	1167	N	LYS	A	270	18.507	60.215	31.145	1.00	38.12	A	N
ATOM	1168	CA	LYS	A	270	19.589	60.740	30.302	1.00	38.51	A	C
ATOM	1169	CB	LYS	A	270	20.511	59.616	29.811	1.00	38.16	A	C
ATOM	1170	CG	LYS	A	270	21.125	58.721	30.874	1.00	41.06	A	C
ATOM	1171	CD	LYS	A	270	22.288	59.391	31.567	1.00	38.38	A	C
ATOM	1172	CE	LYS	A	270	23.088	58.381	32.379	1.00	36.07	A	C
ATOM	1173	NZ	LYS	A	270	24.297	59.001	32.993	1.00	29.99	A	N
ATOM	1174	C	LYS	A	270	18.977	61.397	29.054	1.00	38.60	A	C
ATOM	1175	O	LYS	A	270	18.327	60.714	28.265	1.00	38.86	A	O
ATOM	1176	N	ILE	A	271	19.168	62.702	28.870	1.00	36.85	A	N
ATOM	1177	CA	ILE	A	271	18.641	63.351	27.671	1.00	38.69	A	C
ATOM	1178	CB	ILE	A	271	18.652	64.906	27.752	1.00	38.48	A	C
ATOM	1179	CG2	ILE	A	271	18.141	65.498	26.426	1.00	38.13	A	C
ATOM	1180	CG1	ILE	A	271	17.739	65.390	28.872	1.00	37.28	A	C
ATOM	1181	CD1	ILE	A	271	17.641	66.894	28.965	1.00	41.06	A	C
ATOM	1182	C	ILE	A	271	19.579	62.934	26.547	1.00	39.33	A	C

ATOM	1183	O	ILE	A	271	20.761	63.273	26.562	1.00	33.34	A	O
ATOM	1184	N	ALA	A	272	19.053	62.203	25.575	1.00	43.07	A	N
ATOM	1185	CA	ALA	A	272	19.873	61.721	24.474	1.00	50.47	A	C
ATOM	1186	CB	ALA	A	272	19.121	60.654	23.687	1.00	46.47	A	C
ATOM	1187	C	ALA	A	272	20.320	62.829	23.539	1.00	56.66	A	C
ATOM	1188	O	ALA	A	272	19.630	63.837	23.379	1.00	57.25	A	O
ATOM	1189	N	ASP	A	273	21.490	62.625	22.935	1.00	61.74	A	N
ATOM	1190	CA	ASP	A	273	22.062	63.562	21.979	1.00	65.85	A	C
ATOM	1191	CB	ASP	A	273	23.107	62.837	21.120	1.00	66.61	A	C
ATOM	1192	CG	ASP	A	273	22.680	61.413	20.754	1.00	65.34	A	C
ATOM	1193	OD1	ASP	A	273	22.571	60.579	21.679	1.00	66.75	A	O
ATOM	1194	OD2	ASP	A	273	22.457	61.118	19.561	1.00	64.24	A	O
ATOM	1195	C	ASP	A	273	20.934	64.078	21.095	1.00	69.02	A	C
ATOM	1196	O	ASP	A	273	20.500	63.379	20.175	1.00	69.51	A	O
ATOM	1197	N	PHE	A	274	20.444	65.287	21.365	1.00	72.26	A	N
ATOM	1198	CA	PHE	A	274	19.359	65.784	20.535	1.00	74.92	A	C
ATOM	1199	CB	PHE	A	274	18.873	67.185	20.973	1.00	77.06	A	C
ATOM	1200	CG	PHE	A	274	19.908	68.278	20.889	1.00	78.54	A	C
ATOM	1201	CD1	PHE	A	274	20.908	68.397	21.850	1.00	78.95	A	C
ATOM	1202	CD2	PHE	A	274	19.819	69.250	19.896	1.00	79.45	A	C
ATOM	1203	CE1	PHE	A	274	21.797	69.480	21.823	1.00	79.11	A	C
ATOM	1204	CE2	PHE	A	274	20.700	70.330	19.861	1.00	80.03	A	C
ATOM	1205	CZ	PHE	A	274	21.691	70.448	20.828	1.00	79.54	A	C
ATOM	1206	C	PHE	A	274	19.759	65.753	19.067	1.00	76.11	A	C
ATOM	1207	O	PHE	A	274	20.857	66.162	18.688	1.00	75.92	A	O
ATOM	1208	N	GLY	A	275	18.860	65.208	18.257	1.00	77.26	A	N
ATOM	1209	CA	GLY	A	275	19.106	65.096	16.836	1.00	77.96	A	C
ATOM	1210	C	GLY	A	275	19.590	63.710	16.471	1.00	79.01	A	C
ATOM	1211	O	GLY	A	275	19.492	62.770	17.261	1.00	78.98	A	O
ATOM	1212	N	TRP	A	276	20.137	63.595	15.268	1.00	78.75	A	N
ATOM	1213	CA	TRP	A	276	20.659	62.336	14.751	1.00	77.92	A	C
ATOM	1214	CB	TRP	A	276	21.944	61.930	15.489	1.00	80.84	A	C
ATOM	1215	CG	TRP	A	276	22.633	63.003	16.308	1.00	83.68	A	C
ATOM	1216	CD2	TRP	A	276	23.693	63.869	15.877	1.00	84.50	A	C
ATOM	1217	CE2	TRP	A	276	24.079	64.647	16.994	1.00	84.93	A	C
ATOM	1218	CE3	TRP	A	276	24.355	64.063	14.656	1.00	85.10	A	C
ATOM	1219	CD1	TRP	A	276	22.420	63.289	17.627	1.00	84.53	A	C
ATOM	1220	NE1	TRP	A	276	23.287	64.271	18.047	1.00	85.75	A	N
ATOM	1221	CZ2	TRP	A	276	25.100	65.604	16.928	1.00	85.38	A	C
ATOM	1222	CZ3	TRP	A	276	25.373	65.018	14.592	1.00	85.86	A	C
ATOM	1223	CH2	TRP	A	276	25.732	65.774	15.723	1.00	85.40	A	C
ATOM	1224	C	TRP	A	276	19.696	61.138	14.777	1.00	75.88	A	C
ATOM	1225	O	TRP	A	276	20.148	60.001	14.873	1.00	75.31	A	O
ATOM	1226	N	SER	A	277	18.386	61.363	14.692	1.00	73.54	A	N
ATOM	1227	CA	SER	A	277	17.470	60.218	14.706	1.00	69.92	A	C
ATOM	1228	CB	SER	A	277	16.009	60.656	14.626	1.00	69.39	A	C
ATOM	1229	OG	SER	A	277	15.145	59.528	14.690	1.00	68.26	A	O
ATOM	1230	C	SER	A	277	17.795	59.324	13.518	1.00	68.61	A	C
ATOM	1231	O	SER	A	277	18.330	59.791	12.514	1.00	66.97	A	O
ATOM	1232	N	VAL	A	278	17.460	58.042	13.624	1.00	67.80	A	N
ATOM	1233	CA	VAL	A	278	17.764	57.094	12.560	1.00	67.75	A	C
ATOM	1234	CB	VAL	A	278	18.452	55.830	13.161	1.00	67.67	A	C
ATOM	1235	CG1	VAL	A	278	17.429	54.748	13.454	1.00	66.50	A	C
ATOM	1236	CG2	VAL	A	278	19.530	55.338	12.245	1.00	67.32	A	C
ATOM	1237	C	VAL	A	278	16.554	56.679	11.713	1.00	68.01	A	C
ATOM	1238	O	VAL	A	278	16.722	56.161	10.606	1.00	66.68	A	O
ATOM	1239	N	ALA	A	279	15.351	56.918	12.240	1.00	69.17	A	N
ATOM	1240	CA	ALA	A	279	14.076	56.586	11.584	1.00	69.86	A	C
ATOM	1241	CB	ALA	A	279	14.174	56.772	10.063	1.00	69.92	A	C
ATOM	1242	C	ALA	A	279	13.607	55.167	11.904	1.00	68.92	A	C
ATOM	1243	O	ALA	A	279	13.970	54.593	12.929	1.00	69.04	A	O
ATOM	1244	N	GLY	A	290	10.838	65.378	16.485	1.00	60.42	A	N
ATOM	1245	CA	GLY	A	290	9.748	65.485	17.442	1.00	58.73	A	C
ATOM	1246	C	GLY	A	290	8.433	65.948	16.835	1.00	57.18	A	C
ATOM	1247	O	GLY	A	290	8.400	66.907	16.063	1.00	56.04	A	O
ATOM	1248	N	THR	A	291	7.341	65.281	17.198	1.00	54.45	A	N
ATOM	1249	CA	THR	A	291	6.039	65.646	16.665	1.00	49.75	A	C
ATOM	1250	CB	THR	A	291	4.985	64.552	16.910	1.00	49.00	A	C
ATOM	1251	OG1	THR	A	291	4.825	64.330	18.315	1.00	49.86	A	O
ATOM	1252	CG2	THR	A	291	5.388	63.284	16.227	1.00	51.10	A	C
ATOM	1253	C	THR	A	291	5.471	66.956	17.194	1.00	46.23	A	C
ATOM	1254	O	THR	A	291	5.959	67.548	18.163	1.00	42.68	A	O

ATOM	1255	N	LEU	A	292	4.419	67.386	16.514	1.00	43.51	A	N
ATOM	1256	CA	LEU	A	292	3.696	68.601	16.819	1.00	38.04	A	C
ATOM	1257	CB	LEU	A	292	2.460	68.662	15.927	1.00	35.68	A	C
ATOM	1258	CG	LEU	A	292	1.624	69.937	15.948	1.00	33.83	A	C
ATOM	1259	CD1	LEU	A	292	2.511	71.150	15.696	1.00	33.10	A	C
ATOM	1260	CD2	LEU	A	292	0.550	69.821	14.881	1.00	35.15	A	C
ATOM	1261	C	LEU	A	292	3.275	68.691	18.280	1.00	36.84	A	C
ATOM	1262	O	LEU	A	292	3.286	69.771	18.862	1.00	36.40	A	O
ATOM	1263	N	ASP	A	293	2.910	67.558	18.878	1.00	36.26	A	N
ATOM	1264	CA	ASP	A	293	2.464	67.545	20.270	1.00	33.20	A	C
ATOM	1265	CB	ASP	A	293	2.067	66.132	20.701	1.00	36.86	A	C
ATOM	1266	CG	ASP	A	293	0.647	65.790	20.328	1.00	37.14	A	C
ATOM	1267	OD1	ASP	A	293	0.417	65.413	19.166	1.00	41.08	A	O
ATOM	1268	OD2	ASP	A	293	-0.240	65.910	21.198	1.00	39.86	A	O
ATOM	1269	C	ASP	A	293	3.447	68.091	21.279	1.00	32.18	A	C
ATOM	1270	O	ASP	A	293	3.060	68.442	22.388	1.00	32.05	A	O
ATOM	1271	N	TYR	A	294	4.719	68.170	20.920	1.00	33.09	A	N
ATOM	1272	CA	TYR	A	294	5.692	68.669	21.880	1.00	35.14	A	C
ATOM	1273	CB	TYR	A	294	6.837	67.653	22.027	1.00	36.03	A	C
ATOM	1274	CG	TYR	A	294	6.352	66.274	22.443	1.00	35.56	A	C
ATOM	1275	CD1	TYR	A	294	5.804	65.389	21.509	1.00	35.20	A	C
ATOM	1276	CE1	TYR	A	294	5.310	64.131	21.905	1.00	37.12	A	C
ATOM	1277	CD2	TYR	A	294	6.397	65.872	23.783	1.00	35.96	A	C
ATOM	1278	CE2	TYR	A	294	5.908	64.628	24.184	1.00	34.99	A	C
ATOM	1279	CZ	TYR	A	294	5.369	63.762	23.244	1.00	35.56	A	C
ATOM	1280	OH	TYR	A	294	4.917	62.521	23.644	1.00	35.68	A	O
ATOM	1281	C	TYR	A	294	6.245	70.064	21.566	1.00	37.52	A	C
ATOM	1282	O	TYR	A	294	7.079	70.590	22.303	1.00	39.14	A	O
ATOM	1283	N	LEU	A	295	5.758	70.674	20.493	1.00	36.26	A	N
ATOM	1284	CA	LEU	A	295	6.232	72.005	20.102	1.00	36.64	A	C
ATOM	1285	CB	LEU	A	295	6.135	72.154	18.587	1.00	35.17	A	C
ATOM	1286	CG	LEU	A	295	6.953	71.141	17.781	1.00	36.95	A	C
ATOM	1287	CD1	LEU	A	295	6.675	71.328	16.282	1.00	37.45	A	C
ATOM	1288	CD2	LEU	A	295	8.440	71.326	18.097	1.00	36.23	A	C
ATOM	1289	C	LEU	A	295	5.480	73.161	20.765	1.00	34.99	A	C
ATOM	1290	O	LEU	A	295	4.256	73.170	20.811	1.00	34.10	A	O
ATOM	1291	N	PRO	A	296	6.215	74.154	21.293	1.00	35.03	A	N
ATOM	1292	CD	PRO	A	296	7.683	74.244	21.374	1.00	32.23	A	C
ATOM	1293	CA	PRO	A	296	5.583	75.306	21.939	1.00	34.56	A	C
ATOM	1294	CB	PRO	A	296	6.743	75.963	22.686	1.00	32.65	A	C
ATOM	1295	CG	PRO	A	296	7.897	75.677	21.801	1.00	35.00	A	C
ATOM	1296	C	PRO	A	296	4.980	76.216	20.865	1.00	35.38	A	C
ATOM	1297	O	PRO	A	296	5.423	76.210	19.715	1.00	31.51	A	O
ATOM	1298	N	PRO	A	297	3.964	77.009	21.231	1.00	35.66	A	N
ATOM	1299	CD	PRO	A	297	3.432	77.146	22.597	1.00	35.54	A	C
ATOM	1300	CA	PRO	A	297	3.283	77.927	20.313	1.00	36.80	A	C
ATOM	1301	CB	PRO	A	297	2.400	78.758	21.245	1.00	37.34	A	C
ATOM	1302	CG	PRO	A	297	2.100	77.819	22.358	1.00	38.15	A	C
ATOM	1303	C	PRO	A	297	4.182	78.818	19.458	1.00	37.23	A	C
ATOM	1304	O	PRO	A	297	3.991	78.920	18.235	1.00	33.75	A	O
ATOM	1305	N	GLU	A	298	5.158	79.461	20.095	1.00	37.28	A	N
ATOM	1306	CA	GLU	A	298	6.040	80.368	19.375	1.00	39.04	A	C
ATOM	1307	CB	GLU	A	298	7.016	81.072	20.335	1.00	40.64	A	C
ATOM	1308	CG	GLU	A	298	7.969	80.146	21.080	1.00	41.60	A	C
ATOM	1309	CD	GLU	A	298	7.456	79.749	22.453	1.00	41.95	A	C
ATOM	1310	OE1	GLU	A	298	6.216	79.639	22.633	1.00	37.64	A	O
ATOM	1311	OE2	GLU	A	298	8.304	79.536	23.352	1.00	42.68	A	O
ATOM	1312	C	GLU	A	298	6.805	79.668	18.266	1.00	40.93	A	C
ATOM	1313	O	GLU	A	298	7.175	80.297	17.272	1.00	40.31	A	O
ATOM	1314	N	MET	A	299	7.029	78.366	18.415	1.00	41.73	A	N
ATOM	1315	CA	MET	A	299	7.759	77.624	17.395	1.00	43.83	A	C
ATOM	1316	CB	MET	A	299	8.495	76.437	18.017	1.00	47.01	A	C
ATOM	1317	CG	MET	A	299	9.916	76.769	18.440	1.00	50.51	A	C
ATOM	1318	SD	MET	A	299	10.859	75.322	18.989	1.00	56.33	A	S
ATOM	1319	CE	MET	A	299	10.979	74.398	17.460	1.00	57.30	A	C
ATOM	1320	C	MET	A	299	6.907	77.157	16.222	1.00	45.51	A	C
ATOM	1321	O	MET	A	299	7.357	77.219	15.078	1.00	46.23	A	O
ATOM	1322	N	ILE	A	300	5.686	76.691	16.473	1.00	46.41	A	N
ATOM	1323	CA	ILE	A	300	4.857	76.256	15.354	1.00	49.69	A	C
ATOM	1324	CB	ILE	A	300	3.667	75.376	15.798	1.00	48.42	A	C
ATOM	1325	CG2	ILE	A	300	4.178	74.162	16.561	1.00	47.80	A	C
ATOM	1326	CG1	ILE	A	300	2.709	76.179	16.675	1.00	49.64	A	C

ATOM	1327	CD1	ILE	A	300	1.559	75.360	17.234	1.00	47.41	A	C
ATOM	1328	C	ILE	A	300	4.322	77.478	14.610	1.00	54.06	A	C
ATOM	1329	O	ILE	A	300	4.079	77.416	13.399	1.00	54.63	A	O
ATOM	1330	N	GLU	A	301	4.153	78.590	15.332	1.00	55.66	A	N
ATOM	1331	CA	GLU	A	301	3.646	79.827	14.733	1.00	56.31	A	C
ATOM	1332	CB	GLU	A	301	3.129	80.780	15.815	1.00	54.96	A	C
ATOM	1333	CG	GLU	A	301	1.744	80.422	16.350	1.00	54.86	A	C
ATOM	1334	CD	GLU	A	301	1.408	81.163	17.629	1.00	57.37	A	C
ATOM	1335	OE1	GLU	A	301	2.017	82.225	17.865	1.00	61.01	A	O
ATOM	1336	OE2	GLU	A	301	0.535	80.701	18.397	1.00	57.95	A	O
ATOM	1337	C	GLU	A	301	4.684	80.533	13.875	1.00	56.92	A	C
ATOM	1338	O	GLU	A	301	4.345	81.438	13.120	1.00	60.15	A	O
ATOM	1339	N	GLY	A	302	5.943	80.119	13.988	1.00	58.80	A	N
ATOM	1340	CA	GLY	A	302	6.998	80.729	13.191	1.00	59.94	A	C
ATOM	1341	C	GLY	A	302	7.683	81.921	13.838	1.00	61.59	A	C
ATOM	1342	O	GLY	A	302	8.681	82.429	13.322	1.00	60.55	A	O
ATOM	1343	N	ARG	A	303	7.149	82.359	14.974	1.00	62.63	A	N
ATOM	1344	CA	ARG	A	303	7.688	83.497	15.712	1.00	63.82	A	C
ATOM	1345	CB	ARG	A	303	6.674	83.913	16.778	1.00	64.15	A	C
ATOM	1346	CG	ARG	A	303	5.352	84.320	16.161	1.00	65.61	A	C
ATOM	1347	CD	ARG	A	303	4.180	84.153	17.100	1.00	69.14	A	C
ATOM	1348	NE	ARG	A	303	3.933	85.328	17.925	1.00	72.61	A	N
ATOM	1349	CZ	ARG	A	303	2.797	85.543	18.585	1.00	75.65	A	C
ATOM	1350	NH1	ARG	A	303	2.644	86.641	19.318	1.00	75.84	A	N
ATOM	1351	NH2	ARG	A	303	1.806	84.660	18.509	1.00	75.29	A	N
ATOM	1352	C	ARG	A	303	9.056	83.212	16.339	1.00	64.35	A	C
ATOM	1353	O	ARG	A	303	9.637	82.148	16.122	1.00	65.12	A	O
ATOM	1354	N	MET	A	304	9.572	84.173	17.099	1.00	65.05	A	N
ATOM	1355	CA	MET	A	304	10.871	84.038	17.756	1.00	66.24	A	C
ATOM	1356	CB	MET	A	304	11.377	85.403	18.216	1.00	69.81	A	C
ATOM	1357	CG	MET	A	304	11.911	86.312	17.135	1.00	74.75	A	C
ATOM	1358	SD	MET	A	304	12.200	87.972	17.807	1.00	80.86	A	S
ATOM	1359	CE	MET	A	304	13.387	87.618	19.128	1.00	78.52	A	C
ATOM	1360	C	MET	A	304	10.792	83.139	18.981	1.00	65.57	A	C
ATOM	1361	O	MET	A	304	9.798	83.164	19.710	1.00	66.01	A	O
ATOM	1362	N	HIS	A	305	11.847	82.361	19.216	1.00	64.22	A	N
ATOM	1363	CA	HIS	A	305	11.900	81.478	20.381	1.00	63.54	A	C
ATOM	1364	CB	HIS	A	305	11.502	80.047	20.005	1.00	62.59	A	C
ATOM	1365	CG	HIS	A	305	12.372	79.428	18.958	1.00	63.59	A	C
ATOM	1366	CD2	HIS	A	305	13.509	78.699	19.062	1.00	63.03	A	C
ATOM	1367	ND1	HIS	A	305	12.100	79.524	17.611	1.00	64.03	A	N
ATOM	1368	CE1	HIS	A	305	13.031	78.878	16.930	1.00	64.73	A	C
ATOM	1369	NE2	HIS	A	305	13.897	78.369	17.787	1.00	63.15	A	N
ATOM	1370	C	HIS	A	305	13.284	81.470	21.031	1.00	62.77	A	C
ATOM	1371	O	HIS	A	305	14.303	81.665	20.359	1.00	61.65	A	O
ATOM	1372	N	ASP	A	306	13.307	81.235	22.342	1.00	61.87	A	N
ATOM	1373	CA	ASP	A	306	14.553	81.211	23.109	1.00	59.72	A	C
ATOM	1374	CB	ASP	A	306	14.722	82.543	23.838	1.00	61.31	A	C
ATOM	1375	CG	ASP	A	306	13.804	82.668	25.035	1.00	63.77	A	C
ATOM	1376	OD1	ASP	A	306	12.597	82.368	24.903	1.00	63.61	A	O
ATOM	1377	OD2	ASP	A	306	14.293	83.073	26.111	1.00	67.22	A	O
ATOM	1378	C	ASP	A	306	14.614	80.058	24.128	1.00	57.12	A	C
ATOM	1379	O	ASP	A	306	13.984	79.014	23.944	1.00	55.04	A	O
ATOM	1380	N	GLU	A	307	15.372	80.269	25.202	1.00	53.44	A	N
ATOM	1381	CA	GLU	A	307	15.552	79.274	26.253	1.00	50.60	A	C
ATOM	1382	CB	GLU	A	307	16.547	79.793	27.298	1.00	52.86	A	C
ATOM	1383	CG	GLU	A	307	16.215	81.169	27.862	1.00	56.28	A	C
ATOM	1384	CD	GLU	A	307	15.453	81.128	29.175	1.00	58.72	A	C
ATOM	1385	OE1	GLU	A	307	15.048	82.215	29.646	1.00	62.07	A	O
ATOM	1386	OE2	GLU	A	307	15.264	80.027	29.742	1.00	58.85	A	O
ATOM	1387	C	GLU	A	307	14.259	78.861	26.935	1.00	48.53	A	C
ATOM	1388	O	GLU	A	307	14.153	77.745	27.450	1.00	45.98	A	O
ATOM	1389	N	LYS	A	308	13.275	79.756	26.935	1.00	44.46	A	N
ATOM	1390	CA	LYS	A	308	11.990	79.460	27.555	1.00	42.65	A	C
ATOM	1391	CB	LYS	A	308	11.099	80.706	27.556	1.00	43.53	A	C
ATOM	1392	CG	LYS	A	308	11.596	81.812	28.477	1.00	46.71	A	C
ATOM	1393	CD	LYS	A	308	11.642	81.330	29.916	1.00	46.09	A	C
ATOM	1394	CE	LYS	A	308	12.011	82.458	30.861	1.00	50.52	A	C
ATOM	1395	NZ	LYS	A	308	11.941	82.037	32.292	1.00	48.95	A	N
ATOM	1396	C	LYS	A	308	11.254	78.301	26.881	1.00	39.37	A	C
ATOM	1397	O	LYS	A	308	10.288	77.784	27.439	1.00	38.96	A	O
ATOM	1398	N	VAL	A	309	11.691	77.904	25.685	1.00	37.85	A	N

ATOM	1399	CA	VAL	A	309	11.055	76.781	24.999	1.00	36.62	A	C
ATOM	1400	CB	VAL	A	309	11.665	76.507	23.582	1.00	36.29	A	C
ATOM	1401	CG1	VAL	A	309	11.361	77.654	22.638	1.00	36.56	A	C
ATOM	1402	CG2	VAL	A	309	13.162	76.294	23.680	1.00	36.29	A	C
ATOM	1403	C	VAL	A	309	11.238	75.533	25.873	1.00	36.76	A	C
ATOM	1404	O	VAL	A	309	10.374	74.666	25.902	1.00	37.91	A	O
ATOM	1405	N	ASP	A	310	12.359	75.455	26.594	1.00	36.49	A	N
ATOM	1406	CA	ASP	A	310	12.616	74.311	27.467	1.00	37.02	A	C
ATOM	1407	CB	ASP	A	310	14.048	74.340	28.005	1.00	36.24	A	C
ATOM	1408	CG	ASP	A	310	14.031	74.031	26.947	1.00	39.45	A	C
ATOM	1409	OD1	ASP	A	310	14.820	73.177	26.074	1.00	42.74	A	O
ATOM	1410	OD2	ASP	A	310	16.172	74.629	26.994	1.00	43.52	A	O
ATOM	1411	C	ASP	A	310	11.633	74.227	28.645	1.00	36.95	A	C
ATOM	1412	O	ASP	A	310	11.342	73.133	29.140	1.00	37.49	A	O
ATOM	1413	N	LEU	A	311	11.122	75.365	29.109	1.00	35.08	A	N
ATOM	1414	CA	LEU	A	311	10.166	75.333	30.211	1.00	32.22	A	C
ATOM	1415	CB	LEU	A	311	9.951	76.736	30.790	1.00	34.39	A	C
ATOM	1416	CG	LEU	A	311	10.913	77.158	31.909	1.00	33.96	A	C
ATOM	1417	CD1	LEU	A	311	10.809	76.178	33.064	1.00	35.22	A	C
ATOM	1418	CD2	LEU	A	311	12.334	77.210	31.389	1.00	33.80	A	C
ATOM	1419	C	LEU	A	311	8.833	74.752	29.743	1.00	31.56	A	C
ATOM	1420	O	LEU	A	311	8.139	74.050	30.488	1.00	31.74	A	O
ATOM	1421	N	TRP	A	312	8.466	75.048	28.503	1.00	30.35	A	N
ATOM	1422	CA	TRP	A	312	7.220	74.520	27.960	1.00	29.50	A	C
ATOM	1423	CB	TRP	A	312	6.948	75.139	26.585	1.00	28.53	A	C
ATOM	1424	CG	TRP	A	312	5.759	74.557	25.875	1.00	28.80	A	C
ATOM	1425	CD2	TRP	A	312	4.431	75.100	25.843	1.00	30.03	A	C
ATOM	1426	CE2	TRP	A	312	3.648	74.251	25.027	1.00	29.38	A	C
ATOM	1427	CE3	TRP	A	312	3.830	76.225	26.421	1.00	29.90	A	C
ATOM	1428	CD1	TRP	A	312	5.730	73.429	25.103	1.00	26.36	A	C
ATOM	1429	NE1	TRP	A	312	4.460	73.237	24.589	1.00	30.47	A	N
ATOM	1430	CZ2	TRP	A	312	2.299	74.495	24.775	1.00	32.48	A	C
ATOM	1431	CZ3	TRP	A	312	2.488	76.465	26.171	1.00	31.78	A	C
ATOM	1432	CH2	TRP	A	312	1.739	75.604	25.354	1.00	33.00	A	C
ATOM	1433	C	TRP	A	312	7.319	72.991	27.855	1.00	28.16	A	C
ATOM	1434	O	TRP	A	312	6.371	72.272	28.190	1.00	30.23	A	O
ATOM	1435	N	SER	A	313	8.467	72.503	27.389	1.00	27.71	A	N
ATOM	1436	CA	SER	A	313	8.699	71.066	27.248	1.00	29.31	A	C
ATOM	1437	CB	SER	A	313	10.120	70.803	26.715	1.00	30.43	A	C
ATOM	1438	OG	SER	A	313	10.265	71.217	25.364	1.00	31.34	A	O
ATOM	1439	C	SER	A	313	8.540	70.373	28.605	1.00	30.79	A	C
ATOM	1440	O	SER	A	313	7.926	69.314	28.729	1.00	31.14	A	O
ATOM	1441	N	LEU	A	314	9.101	70.994	29.628	1.00	32.96	A	N
ATOM	1442	CA	LEU	A	314	9.026	70.455	30.966	1.00	33.68	A	C
ATOM	1443	CB	LEU	A	314	9.746	71.412	31.921	1.00	35.73	A	C
ATOM	1444	CG	LEU	A	314	10.693	70.816	32.958	1.00	39.36	A	C
ATOM	1445	CD1	LEU	A	314	11.611	69.795	32.312	1.00	37.79	A	C
ATOM	1446	CD2	LEU	A	314	11.494	71.940	33.611	1.00	39.93	A	C
ATOM	1447	C	LEU	A	314	7.567	70.265	31.368	1.00	34.08	A	C
ATOM	1448	O	LEU	A	314	7.213	69.270	32.002	1.00	35.54	A	O
ATOM	1449	N	GLY	A	315	6.715	71.212	30.974	1.00	34.46	A	N
ATOM	1450	CA	GLY	A	315	5.302	71.129	31.311	1.00	32.61	A	C
ATOM	1451	C	GLY	A	315	4.533	70.037	30.580	1.00	32.40	A	C
ATOM	1452	O	GLY	A	315	3.653	69.393	31.156	1.00	31.59	A	O
ATOM	1453	N	VAL	A	316	4.848	69.839	29.305	1.00	30.85	A	N
ATOM	1454	CA	VAL	A	316	4.191	68.812	28.500	1.00	30.81	A	C
ATOM	1455	CB	VAL	A	316	4.675	68.870	27.019	1.00	31.13	A	C
ATOM	1456	CG1	VAL	A	316	4.091	67.703	26.225	1.00	31.52	A	C
ATOM	1457	CG2	VAL	A	316	4.268	70.206	26.381	1.00	31.54	A	C
ATOM	1458	C	VAL	A	316	4.541	67.431	29.076	1.00	30.12	A	C
ATOM	1459	O	VAL	A	316	3.694	66.547	29.151	1.00	28.42	A	O
ATOM	1460	N	LEU	A	317	5.800	67.269	29.472	1.00	30.58	A	N
ATOM	1461	CA	LEU	A	317	6.307	66.018	30.041	1.00	32.76	A	C
ATOM	1462	CB	LEU	A	317	7.834	66.091	30.182	1.00	33.36	A	C
ATOM	1463	CG	LEU	A	317	8.741	65.504	29.091	1.00	37.19	A	C
ATOM	1464	CD1	LEU	A	317	7.959	65.186	27.838	1.00	34.20	A	C
ATOM	1465	CD2	LEU	A	317	9.868	66.471	28.805	1.00	29.92	A	C
ATOM	1466	C	LEU	A	317	5.700	65.710	31.408	1.00	32.08	A	C
ATOM	1467	O	LEU	A	317	5.249	64.587	31.656	1.00	34.68	A	O
ATOM	1468	N	CYS	A	318	5.702	66.697	32.298	1.00	31.11	A	N
ATOM	1469	CA	CYS	A	318	5.151	66.491	33.629	1.00	33.57	A	C
ATOM	1470	CB	CYS	A	318	5.156	67.798	34.432	1.00	33.30	A	C

	ATOM	1471	SG	CYS	A	318	4.864	67.562	36.226	1.00	37.22	A	S
	ATOM	1472	C	CYS	A	318	3.725	65.973	33.468	1.00	35.37	A	C
	ATOM	1473	O	CYS	A	318	3.326	64.971	34.075	1.00	33.70	A	O
	ATOM	1474	N	TYR	A	319	2.969	66.645	32.613	1.00	32.86	A	N
5	ATOM	1475	CA	TYR	A	319	1.598	66.244	32.364	1.00	33.70	A	C
	ATOM	1476	CB	TYR	A	319	0.927	67.239	31.395	1.00	29.85	A	C
	ATOM	1477	CG	TYR	A	319	-0.525	66.932	31.098	1.00	30.41	A	C
	ATOM	1478	CD1	TYR	A	319	-0.877	65.857	30.276	1.00	28.02	A	C
	ATOM	1479	CE1	TYR	A	319	-2.207	65.545	30.022	1.00	29.18	A	C
10	ATOM	1480	CD2	TYR	A	319	-1.557	67.696	31.667	1.00	28.95	A	C
	ATOM	1481	CE2	TYR	A	319	-2.902	67.387	31.424	1.00	27.56	A	C
	ATOM	1482	CZ	TYR	A	319	-3.217	66.318	30.599	1.00	30.05	A	C
	ATOM	1483	OH	TYR	A	319	-4.530	66.032	30.309	1.00	30.26	A	O
	ATOM	1484	C	TYR	A	319	1.550	64.825	31.796	1.00	33.79	A	C
15	ATOM	1485	O	TYR	A	319	0.804	63.970	32.286	1.00	34.68	A	O
	ATOM	1486	N	GLU	A	320	2.343	64.562	30.764	1.00	34.53	A	N
	ATOM	1487	CA	GLU	A	320	2.317	63.236	30.153	1.00	34.32	A	C
	ATOM	1488	CB	GLU	A	320	3.228	63.166	28.927	1.00	31.06	A	C
	ATOM	1489	CG	GLU	A	320	3.005	61.857	28.188	1.00	40.04	A	C
20	ATOM	1490	CD	GLU	A	320	3.781	61.719	26.906	1.00	42.41	A	C
	ATOM	1491	OE1	GLU	A	320	3.546	60.713	26.203	1.00	44.86	A	O
	ATOM	1492	OE2	GLU	A	320	4.618	62.591	26.600	1.00	43.17	A	O
	ATOM	1493	C	GLU	A	320	2.688	62.104	31.116	1.00	32.80	A	C
	ATOM	1494	O	GLU	A	320	2.109	61.018	31.045	1.00	32.14	A	O
25	ATOM	1495	N	PHE	A	321	3.651	62.357	32.003	1.00	32.51	A	N
	ATOM	1496	CA	PHE	A	321	4.071	61.343	32.973	1.00	33.85	A	C
	ATOM	1497	CB	PHE	A	321	5.235	61.833	33.829	1.00	29.43	A	C
	ATOM	1498	CG	PHE	A	321	6.517	62.054	33.070	1.00	30.26	A	C
	ATOM	1499	CD1	PHE	A	321	6.711	61.505	31.816	1.00	28.99	A	C
30	ATOM	1500	CD2	PHE	A	321	7.556	62.764	33.655	1.00	25.23	A	C
	ATOM	1501	CE1	PHE	A	321	7.932	61.654	31.156	1.00	32.51	A	C
	ATOM	1502	CE2	PHE	A	321	8.782	62.919	33.007	1.00	30.02	A	C
	ATOM	1503	CZ	PHE	A	321	8.969	62.356	31.750	1.00	28.27	A	C
	ATOM	1504	C	PHE	A	321	2.933	60.969	33.916	1.00	36.33	A	C
35	ATOM	1505	O	PHE	A	321	2.740	59.800	34.239	1.00	34.14	A	O
	ATOM	1506	N	LEU	A	322	2.191	61.976	34.367	1.00	37.42	A	N
	ATOM	1507	CA	LEU	A	322	1.085	61.755	35.296	1.00	37.42	A	C
	ATOM	1508	CB	LEU	A	322	0.811	63.030	36.085	1.00	38.07	A	C
	ATOM	1509	CG	LEU	A	322	1.884	63.502	37.050	1.00	37.46	A	C
40	ATOM	1510	CD1	LEU	A	322	1.563	64.921	37.490	1.00	41.27	A	C
	ATOM	1511	CD2	LEU	A	322	1.939	62.557	38.246	1.00	40.08	A	C
	ATOM	1512	C	LEU	A	322	-0.214	61.302	34.658	1.00	37.12	A	C
	ATOM	1513	O	LEU	A	322	-1.004	60.596	35.281	1.00	38.55	A	O
	ATOM	1514	N	VAL	A	323	-0.435	61.692	33.410	1.00	38.25	A	N
45	ATOM	1515	CA	VAL	A	323	-1.686	61.356	32.743	1.00	37.24	A	C
	ATOM	1516	CB	VAL	A	323	-2.283	62.634	32.058	1.00	35.89	A	C
	ATOM	1517	CG1	VAL	A	323	-3.556	62.300	31.285	1.00	35.08	A	C
	ATOM	1518	CG2	VAL	A	323	-2.587	63.683	33.123	1.00	33.83	A	C
	ATOM	1519	C	VAL	A	323	-1.609	60.209	31.746	1.00	37.69	A	C
50	ATOM	1520	O	VAL	A	323	-2.620	59.538	31.493	1.00	38.39	A	O
	ATOM	1521	N	GLY	A	324	-0.429	59.972	31.177	1.00	36.52	A	N
	ATOM	1522	CA	GLY	A	324	-0.310	58.887	30.215	1.00	38.42	A	C
	ATOM	1523	C	GLY	A	324	-0.333	59.333	28.759	1.00	39.62	A	C
	ATOM	1524	O	GLY	A	324	-0.077	58.536	27.855	1.00	36.81	A	O
55	ATOM	1525	N	LYS	A	325	-0.652	60.606	28.527	1.00	40.00	A	N
	ATOM	1526	CA	LYS	A	325	-0.682	61.165	27.173	1.00	37.45	A	C
	ATOM	1527	CB	LYS	A	325	-2.002	60.824	26.477	1.00	39.47	A	C
	ATOM	1528	CG	LYS	A	325	-3.252	61.105	27.288	1.00	42.40	A	C
	ATOM	1529	CD	LYS	A	325	-4.497	60.695	26.509	1.00	45.48	A	C
60	ATOM	1530	CE	LYS	A	325	-5.785	61.028	27.265	1.00	49.79	A	C
	ATOM	1531	NZ	LYS	A	325	-5.968	60.179	28.489	1.00	55.16	A	N
	ATOM	1532	C	LYS	A	325	-0.449	62.675	27.230	1.00	33.68	A	C
	ATOM	1533	O	LYS	A	325	-0.751	63.318	28.236	1.00	31.87	A	O
	ATOM	1534	N	PRO	A	326	0.121	63.256	26.158	1.00	31.60	A	N
65	ATOM	1535	CD	PRO	A	326	0.475	62.618	24.876	1.00	32.20	A	C
	ATOM	1536	CA	PRO	A	326	0.390	64.697	26.133	1.00	31.72	A	C
	ATOM	1537	CB	PRO	A	326	1.174	64.879	24.832	1.00	31.00	A	C
	ATOM	1538	CG	PRO	A	326	0.629	63.796	23.948	1.00	32.88	A	C
	ATOM	1539	C	PRO	A	326	-0.903	65.527	26.234	1.00	29.94	A	C
70	ATOM	1540	O	PRO	A	326	-1.946	65.112	25.753	1.00	30.57	A	O
	ATOM	1541	N	PRO	A	327	-0.836	66.715	26.857	1.00	27.73	A	N
	ATOM	1542	CD	PRO	A	327	0.377	67.360	27.400	1.00	27.90	A	C

ATOM	1543	CA	PRO	A	327	-2.024	67.570	27.025	1.00	29.32	A	C
ATOM	1544	CB	PRO	A	327	-1.517	68.695	27.933	1.00	25.30	A	C
ATOM	1545	CG	PRO	A	327	-0.039	68.828	27.530	1.00	27.21	A	C
ATOM	1546	C	PRO	A	327	-2.821	68.110	25.831	1.00	30.82	A	C
ATOM	1547	O	PRO	A	327	-3.998	68.441	25.988	1.00	33.12	A	O
ATOM	1548	N	PHE	A	328	-2.218	68.177	24.649	1.00	31.39	A	N
ATOM	1549	CA	PHE	A	328	-2.901	68.742	23.486	1.00	33.88	A	C
ATOM	1550	CB	PHE	A	328	-2.041	69.869	22.890	1.00	33.58	A	C
ATOM	1551	CG	PHE	A	328	-1.601	70.894	23.899	1.00	33.55	A	C
ATOM	1552	CD1	PHE	A	328	-2.531	71.726	24.522	1.00	33.79	A	C
ATOM	1553	CD2	PHE	A	328	-0.257	71.002	24.256	1.00	33.06	A	C
ATOM	1554	CE1	PHE	A	328	-2.133	72.647	25.490	1.00	33.48	A	C
ATOM	1555	CE2	PHE	A	328	0.160	71.923	25.226	1.00	34.56	A	C
ATOM	1556	CZ	PHE	A	328	-0.781	72.748	25.846	1.00	36.22	A	C
ATOM	1557	C	PHE	A	328	-3.240	67.739	22.390	1.00	36.41	A	C
ATOM	1558	O	PHE	A	328	-3.555	68.125	21.260	1.00	36.68	A	O
ATOM	1559	N	GLU	A	329	-3.189	66.457	22.728	1.00	39.55	A	N
ATOM	1560	CA	GLU	A	329	-3.457	65.388	21.771	1.00	42.10	A	C
ATOM	1561	CB	GLU	A	329	-3.331	64.037	22.474	1.00	44.65	A	C
ATOM	1562	CG	GLU	A	329	-3.295	62.852	21.537	1.00	51.26	A	C
ATOM	1563	CD	GLU	A	329	-2.954	61.571	22.264	1.00	54.01	A	C
ATOM	1564	OE1	GLU	A	329	-3.729	61.174	23.160	1.00	56.26	A	O
ATOM	1565	OE2	GLU	A	329	-1.907	60.966	21.943	1.00	57.24	A	O
ATOM	1566	C	GLU	A	329	-4.820	65.498	21.089	1.00	41.21	A	C
ATOM	1567	O	GLU	A	329	-5.827	65.795	21.731	1.00	38.95	A	O
ATOM	1568	N	ALA	A	330	-4.842	65.248	19.783	1.00	41.49	A	N
ATOM	1569	CA	ALA	A	330	-6.077	65.330	19.014	1.00	44.78	A	C
ATOM	1570	CB	ALA	A	330	-6.345	66.782	18.609	1.00	45.23	A	C
ATOM	1571	C	ALA	A	330	-6.059	64.438	17.775	1.00	45.72	A	C
ATOM	1572	O	ALA	A	330	-5.013	63.941	17.363	1.00	45.07	A	O
ATOM	1573	N	ASN	A	331	-7.234	64.252	17.185	1.00	47.77	A	N
ATOM	1574	CA	ASN	A	331	-7.386	63.413	16.006	1.00	50.88	A	C
ATOM	1575	CB	ASN	A	331	-8.875	63.131	15.755	1.00	54.96	A	C
ATOM	1576	CG	ASN	A	331	-9.508	62.298	16.865	1.00	60.45	A	C
ATOM	1577	OD1	ASN	A	331	-9.016	61.216	17.202	1.00	64.11	A	O
ATOM	1578	ND2	ASN	A	331	-10.608	62.795	17.433	1.00	63.29	A	N
ATOM	1579	C	ASN	A	331	-6.749	63.980	14.741	1.00	49.91	A	C
ATOM	1580	O	ASN	A	331	-6.409	63.229	13.833	1.00	51.49	A	O
ATOM	1581	N	THR	A	332	-6.586	65.296	14.675	1.00	48.66	A	N
ATOM	1582	CA	THR	A	332	-5.982	65.917	13.496	1.00	46.76	A	C
ATOM	1583	CB	THR	A	332	-7.050	66.648	12.650	1.00	47.96	A	C
ATOM	1584	OG1	THR	A	332	-7.648	67.696	13.424	1.00	45.93	A	O
ATOM	1585	CG2	THR	A	332	-8.131	65.675	12.217	1.00	46.55	A	C
ATOM	1586	C	THR	A	332	-4.886	66.914	13.864	1.00	44.80	A	C
ATOM	1587	O	THR	A	332	-4.875	67.444	14.973	1.00	41.95	A	O
ATOM	1588	N	TYR	A	333	-3.954	67.155	12.940	1.00	43.86	A	N
ATOM	1589	CA	TYR	A	333	-2.885	68.115	13.199	1.00	43.43	A	C
ATOM	1590	CB	TYR	A	333	-1.938	68.232	11.999	1.00	47.91	A	C
ATOM	1591	CG	TYR	A	333	-1.084	67.015	11.710	1.00	50.72	A	C
ATOM	1592	CD1	TYR	A	333	-1.606	65.916	11.033	1.00	53.76	A	C
ATOM	1593	CE1	TYR	A	333	-0.816	64.803	10.748	1.00	54.63	A	C
ATOM	1594	CD2	TYR	A	333	0.254	66.973	12.099	1.00	50.61	A	C
ATOM	1595	CE2	TYR	A	333	1.053	65.868	11.821	1.00	51.32	A	C
ATOM	1596	CZ	TYR	A	333	0.515	64.786	11.142	1.00	53.90	A	C
ATOM	1597	OH	TYR	A	333	1.305	63.696	10.836	1.00	52.72	A	O
ATOM	1598	C	TYR	A	333	-3.561	69.470	13.416	1.00	42.37	A	C
ATOM	1599	O	TYR	A	333	-3.083	70.317	14.169	1.00	39.21	A	O
ATOM	1600	N	GLN	A	334	-4.688	69.643	12.734	1.00	41.68	A	N
ATOM	1601	CA	GLN	A	334	-5.479	70.865	12.790	1.00	41.47	A	C
ATOM	1602	CB	GLN	A	334	-6.709	70.733	11.885	1.00	42.29	A	C
ATOM	1603	CG	GLN	A	334	-7.485	72.011	11.777	1.00	45.81	A	C
ATOM	1604	CD	GLN	A	334	-6.550	73.173	11.567	1.00	51.49	A	C
ATOM	1605	OE1	GLN	A	334	-5.725	73.152	10.653	1.00	52.23	A	O
ATOM	1606	NE2	GLN	A	334	-6.655	74.192	12.420	1.00	52.56	A	N
ATOM	1607	C	GLN	A	334	-5.933	71.195	14.202	1.00	37.45	A	C
ATOM	1608	O	GLN	A	334	-5.690	72.291	14.706	1.00	33.84	A	O
ATOM	1609	N	GLU	A	335	-6.599	70.231	14.821	1.00	35.59	A	N
ATOM	1610	CA	GLU	A	335	-7.113	70.385	16.164	1.00	37.26	A	C
ATOM	1611	CB	GLU	A	335	-8.091	69.243	16.458	1.00	39.04	A	C
ATOM	1612	CG	GLU	A	335	-8.854	69.370	17.767	1.00	44.38	A	C
ATOM	1613	CD	GLU	A	335	-9.901	70.478	17.746	1.00	49.56	A	C
ATOM	1614	OE1	GLU	A	335	-10.579	70.666	18.784	1.00	48.54	A	O

ATOM	1615	OE2	GLU	A	335	-10.042	71.159	16.699	1.00	49.52	A	O
ATOM	1616	C	GLU	A	335	-5.967	70.416	17.189	1.00	36.13	A	C
ATOM	1617	O	GLU	A	335	-6.083	71.062	18.232	1.00	35.59	A	O
ATOM	1618	N	THR	A	336	-4.864	69.723	16.900	1.00	33.83	A	N
ATOM	1619	CA	THR	A	336	-3.721	69.727	17.819	1.00	32.60	A	C
ATOM	1620	CB	THR	A	336	-2.606	68.755	17.357	1.00	31.68	A	C
ATOM	1621	OG1	THR	A	336	-3.126	67.422	17.292	1.00	34.29	A	O
ATOM	1622	CG2	THR	A	336	-1.443	68.771	18.331	1.00	29.91	A	C
ATOM	1623	C	THR	A	336	-3.143	71.145	17.889	1.00	31.31	A	C
ATOM	1624	O	THR	A	336	-2.914	71.686	18.971	1.00	28.38	A	O
ATOM	1625	N	TYR	A	337	-2.911	71.732	16.717	1.00	31.54	A	N
ATOM	1626	CA	TYR	A	337	-2.381	73.094	16.597	1.00	33.23	A	C
ATOM	1627	CB	TYR	A	337	-2.339	73.489	15.120	1.00	38.97	A	C
ATOM	1628	CG	TYR	A	337	-1.770	74.861	14.855	1.00	43.55	A	C
ATOM	1629	CD1	TYR	A	337	-0.414	75.030	14.589	1.00	50.62	A	C
ATOM	1630	CE1	TYR	A	337	0.123	76.290	14.343	1.00	53.16	A	C
ATOM	1631	CD2	TYR	A	337	-2.584	75.991	14.872	1.00	43.59	A	C
ATOM	1632	CE2	TYR	A	337	-2.062	77.254	14.632	1.00	47.84	A	C
ATOM	1633	CZ	TYR	A	337	-0.704	77.397	14.364	1.00	53.57	A	C
ATOM	1634	OH	TYR	A	337	-0.170	78.637	14.096	1.00	56.75	A	O
ATOM	1635	C	TYR	A	337	-3.290	74.070	17.359	1.00	32.20	A	C
ATOM	1636	O	TYR	A	337	-2.823	74.890	18.159	1.00	30.91	A	O
ATOM	1637	N	LYS	A	338	-4.592	73.966	17.103	1.00	30.03	A	N
ATOM	1638	CA	LYS	A	338	-5.580	74.809	17.771	1.00	30.11	A	C
ATOM	1639	CB	LYS	A	338	-7.008	74.344	17.421	1.00	31.44	A	C
ATOM	1640	CG	LYS	A	338	-8.107	75.329	17.852	1.00	34.97	A	C
ATOM	1641	CD	LYS	A	338	-9.521	74.720	17.889	1.00	38.62	A	C
ATOM	1642	CE	LYS	A	338	-10.082	74.415	16.504	1.00	43.83	A	C
ATOM	1643	NZ	LYS	A	338	-11.532	74.025	16.552	1.00	43.82	A	N
ATOM	1644	C	LYS	A	338	-5.387	74.764	19.289	1.00	30.09	A	C
ATOM	1645	O	LYS	A	338	-5.257	75.804	19.942	1.00	29.38	A	O
ATOM	1646	N	ARG	A	339	-5.356	73.554	19.846	1.00	29.91	A	N
ATOM	1647	CA	ARG	A	339	-5.200	73.370	21.288	1.00	29.88	A	C
ATOM	1648	CB	ARG	A	339	-5.376	71.880	21.642	1.00	32.35	A	C
ATOM	1649	CG	ARG	A	339	-6.790	71.364	21.347	1.00	37.87	A	C
ATOM	1650	CD	ARG	A	339	-6.962	69.849	21.524	1.00	43.23	A	C
ATOM	1651	NE	ARG	A	339	-8.337	69.455	21.193	1.00	48.29	A	N
ATOM	1652	CZ	ARG	A	339	-8.845	68.223	21.287	1.00	50.25	A	C
ATOM	1653	NH1	ARG	A	339	-8.107	67.202	21.712	1.00	48.72	A	N
ATOM	1654	NH2	ARG	A	339	-10.111	68.010	20.940	1.00	51.23	A	N
ATOM	1655	C	ARG	A	339	-3.883	73.906	21.850	1.00	28.91	A	C
ATOM	1656	O	ARG	A	339	-3.853	74.491	22.930	1.00	31.71	A	O
ATOM	1657	N	ILE	A	340	-2.792	73.700	21.125	1.00	28.62	A	N
ATOM	1658	CA	ILE	A	340	-1.487	74.180	21.565	1.00	30.14	A	C
ATOM	1659	CB	ILE	A	340	-0.366	73.660	20.631	1.00	28.04	A	C
ATOM	1660	CG2	ILE	A	340	0.932	74.397	20.925	1.00	25.58	A	C
ATOM	1661	CG1	ILE	A	340	-0.190	72.142	20.807	1.00	26.16	A	C
ATOM	1662	CD1	ILE	A	340	0.830	71.531	19.845	1.00	27.76	A	C
ATOM	1663	C	ILE	A	340	-1.462	75.712	21.526	1.00	32.65	A	C
ATOM	1664	O	ILE	A	340	-1.024	76.377	22.470	1.00	33.37	A	O
ATOM	1665	N	SER	A	341	-1.935	76.243	20.404	1.00	33.83	A	N
ATOM	1666	CA	SER	A	341	-2.000	77.676	20.138	1.00	35.56	A	C
ATOM	1667	CB	SER	A	341	-2.644	77.892	18.772	1.00	35.09	A	C
ATOM	1668	OG	SER	A	341	-1.991	78.931	18.084	1.00	39.44	A	O
ATOM	1669	C	SER	A	341	-2.794	78.436	21.185	1.00	35.59	A	C
ATOM	1670	O	SER	A	341	-2.367	79.478	21.673	1.00	37.28	A	O
ATOM	1671	N	ARG	A	342	-3.952	77.893	21.530	1.00	34.73	A	N
ATOM	1672	CA	ARG	A	342	-4.851	78.508	22.493	1.00	34.53	A	C
ATOM	1673	CB	ARG	A	342	-6.296	78.295	22.016	1.00	35.36	A	C
ATOM	1674	CG	ARG	A	342	-6.539	78.913	20.641	1.00	33.27	A	C
ATOM	1675	CD	ARG	A	342	-7.836	78.460	19.969	1.00	38.01	A	C
ATOM	1676	NE	ARG	A	342	-8.038	79.214	18.730	1.00	41.54	A	N
ATOM	1677	CZ	ARG	A	342	-9.135	79.184	17.974	1.00	41.67	A	C
ATOM	1678	NH1	ARG	A	342	-9.187	79.922	16.870	1.00	44.15	A	N
ATOM	1679	NH2	ARG	A	342	-10.176	78.435	18.315	1.00	37.28	A	N
ATOM	1680	C	ARG	A	342	-4.652	77.962	23.900	1.00	36.18	A	C
ATOM	1681	O	ARG	A	342	-5.446	78.252	24.802	1.00	34.08	A	O
ATOM	1682	N	VAL	A	343	-3.582	77.178	24.072	1.00	35.22	A	N
ATOM	1683	CA	VAL	A	343	-3.221	76.575	25.355	1.00	34.16	A	C
ATOM	1684	CB	VAL	A	343	-2.613	77.622	26.315	1.00	34.38	A	C
ATOM	1685	CG1	VAL	A	343	-2.081	76.935	27.561	1.00	36.51	A	C
ATOM	1686	CG2	VAL	A	343	-1.500	78.391	25.632	1.00	31.25	A	C

ATOM	1687	C	VAL	A	343	-4.441	75.952	26.018	1.00	34.20	A	C
ATOM	1688	O	VAL	A	343	-4.782	76.284	27.153	1.00	31.68	A	O
ATOM	1689	N	GLU	A	344	-5.097	75.050	25.294	1.00	33.81	A	N
ATOM	1690	CA	GLU	A	344	-6.292	74.369	25.783	1.00	34.08	A	C
ATOM	1691	CB	GLU	A	344	-7.340	74.265	24.658	1.00	34.89	A	C
ATOM	1692	CG	GLU	A	344	-8.047	75.572	24.334	1.00	38.33	A	C
ATOM	1693	CD	GLU	A	344	-8.665	75.594	22.944	1.00	40.26	A	C
ATOM	1694	OE1	GLU	A	344	-9.402	76.553	22.636	1.00	39.02	A	O
ATOM	1695	OE2	GLU	A	344	-8.406	74.665	22.154	1.00	41.41	A	O
ATOM	1696	C	GLU	A	344	-6.922	72.972	26.337	1.00	33.90	A	C
ATOM	1697	O	GLU	A	344	-5.887	72.020	25.575	1.00	35.23	A	O
ATOM	1698	N	PHE	A	345	-5.958	72.851	27.661	1.00	35.80	A	N
ATOM	1699	CA	PHE	A	345	-5.736	71.558	28.314	1.00	37.65	A	C
ATOM	1700	CB	PHE	A	345	-4.247	71.370	28.643	1.00	35.66	A	C
ATOM	1701	CG	PHE	A	345	-3.731	72.296	29.714	1.00	38.52	A	C
ATOM	1702	CD1	PHE	A	345	-3.768	71.924	31.052	1.00	40.34	A	C
ATOM	1703	CD2	PHE	A	345	-3.212	73.545	29.382	1.00	38.83	A	C
ATOM	1704	CE1	PHE	A	345	-3.294	72.786	32.049	1.00	41.72	A	C
ATOM	1705	CE2	PHE	A	345	-2.737	74.414	30.361	1.00	39.94	A	C
ATOM	1706	CZ	PHE	A	345	-2.778	74.034	31.701	1.00	43.18	A	C
ATOM	1707	C	PHE	A	345	-6.559	71.455	29.595	1.00	39.42	A	C
ATOM	1708	O	PHE	A	345	-6.876	72.478	30.211	1.00	40.64	A	O
ATOM	1709	N	THR	A	346	-6.905	70.225	29.985	1.00	38.79	A	N
ATOM	1710	CA	THR	A	346	-7.669	69.967	31.209	1.00	38.83	A	C
ATOM	1711	CB	THR	A	346	-9.177	69.732	30.906	1.00	38.24	A	C
ATOM	1712	OG1	THR	A	346	-9.324	68.712	29.912	1.00	35.72	A	O
ATOM	1713	CG2	THR	A	346	-9.831	71.024	30.411	1.00	38.59	A	C
ATOM	1714	C	THR	A	346	-7.103	68.743	31.957	1.00	40.45	A	C
ATOM	1715	O	THR	A	346	-6.477	67.872	31.350	1.00	40.52	A	O
ATOM	1716	N	PHE	A	347	-7.337	68.684	33.267	1.00	38.41	A	N
ATOM	1717	CA	PHE	A	347	-6.832	67.602	34.117	1.00	38.01	A	C
ATOM	1718	CB	PHE	A	347	-6.299	68.175	35.430	1.00	33.25	A	C
ATOM	1719	CG	PHE	A	347	-5.179	69.157	35.272	1.00	37.35	A	C
ATOM	1720	CD1	PHE	A	347	-3.910	68.736	34.870	1.00	36.75	A	C
ATOM	1721	CD2	PHE	A	347	-5.377	70.507	35.570	1.00	35.58	A	C
ATOM	1722	CE1	PHE	A	347	-2.854	69.647	34.773	1.00	37.99	A	C
ATOM	1723	CE2	PHE	A	347	-4.334	71.420	35.477	1.00	36.58	A	C
ATOM	1724	CZ	PHE	A	347	-3.064	70.993	35.077	1.00	36.04	A	C
ATOM	1725	C	PHE	A	347	-7.829	66.501	34.502	1.00	40.55	A	C
ATOM	1726	O	PHE	A	347	-8.996	66.775	34.800	1.00	40.32	A	O
ATOM	1727	N	PRO	A	348	-7.381	65.230	34.493	1.00	42.22	A	N
ATOM	1728	CD	PRO	A	348	-6.184	64.654	33.855	1.00	40.80	A	C
ATOM	1729	CA	PRO	A	348	-8.326	64.177	34.887	1.00	43.29	A	C
ATOM	1730	CB	PRO	A	348	-7.552	62.888	34.612	1.00	41.59	A	C
ATOM	1731	CG	PRO	A	348	-6.671	63.267	33.455	1.00	41.69	A	C
ATOM	1732	C	PRO	A	348	-8.540	64.420	36.380	1.00	43.20	A	C
ATOM	1733	O	PRO	A	348	-7.758	65.136	37.003	1.00	42.10	A	O
ATOM	1734	N	ASP	A	349	-9.574	63.832	36.963	1.00	46.66	A	N
ATOM	1735	CA	ASP	A	349	-9.842	64.058	38.380	1.00	49.33	A	C
ATOM	1736	CB	ASP	A	349	-11.171	63.396	38.774	1.00	52.46	A	C
ATOM	1737	CG	ASP	A	349	-12.363	64.001	38.043	1.00	56.47	A	C
ATOM	1738	OD1	ASP	A	349	-12.403	65.242	37.898	1.00	56.97	A	O
ATOM	1739	OD2	ASP	A	349	-13.265	63.240	37.623	1.00	59.92	A	O
ATOM	1740	C	ASP	A	349	-8.747	63.646	39.375	1.00	49.27	A	C
ATOM	1741	O	ASP	A	349	-8.651	64.225	40.454	1.00	48.92	A	O
ATOM	1742	N	PHE	A	350	-7.908	62.675	39.020	1.00	49.30	A	N
ATOM	1743	CA	PHE	A	350	-6.863	62.219	39.946	1.00	47.22	A	C
ATOM	1744	CB	PHE	A	350	-6.440	60.781	39.598	1.00	46.74	A	C
ATOM	1745	CG	PHE	A	350	-5.715	60.649	38.287	1.00	43.91	A	C
ATOM	1746	CD1	PHE	A	350	-4.417	61.141	38.135	1.00	44.25	A	C
ATOM	1747	CD2	PHE	A	350	-6.330	60.039	37.202	1.00	40.16	A	C
ATOM	1748	CE1	PHE	A	350	-3.748	61.025	36.915	1.00	42.32	A	C
ATOM	1749	CE2	PHE	A	350	-5.674	59.919	35.984	1.00	39.67	A	C
ATOM	1750	CZ	PHE	A	350	-4.382	60.413	35.839	1.00	40.57	A	C
ATOM	1751	C	PHE	A	350	-5.614	63.085	40.109	1.00	47.01	A	C
ATOM	1752	O	PHE	A	350	-4.843	62.876	41.041	1.00	46.65	A	O
ATOM	1753	N	VAL	A	351	-5.395	64.051	39.222	1.00	46.50	A	N
ATOM	1754	CA	VAL	A	351	-4.211	64.893	39.355	1.00	45.42	A	C
ATOM	1755	CB	VAL	A	351	-3.936	65.695	38.057	1.00	44.39	A	C
ATOM	1756	CG1	VAL	A	351	-2.726	66.586	38.236	1.00	40.46	A	C
ATOM	1757	CG2	VAL	A	351	-3.705	64.745	36.909	1.00	42.44	A	C
ATOM	1758	C	VAL	A	351	-4.356	65.847	40.542	1.00	48.95	A	C

ATOM	1759	O	VAL	A	351	-5.391	66.498	40.709	1.00	49.11	A	O
ATOM	1760	N	THR	A	352	-3.304	65.913	41.355	1.00	48.97	A	N
ATOM	1761	CA	THR	A	352	-3.246	66.739	42.557	1.00	50.49	A	C
ATOM	1762	CB	THR	A	352	-2.058	66.288	43.442	1.00	51.76	A	C
ATOM	1763	OG1	THR	A	352	-2.329	64.978	43.962	1.00	54.65	A	O
ATOM	1764	CG2	THR	A	352	-1.839	67.249	44.600	1.00	55.96	A	C
ATOM	1765	C	THR	A	352	-3.127	68.239	42.291	1.00	51.36	A	C
ATOM	1766	O	THR	A	352	-2.633	68.655	41.240	1.00	51.12	A	O
ATOM	1767	N	GLU	A	353	-3.574	69.044	43.256	1.00	49.74	A	N
ATOM	1768	CA	GLU	A	353	-3.519	70.499	43.132	1.00	51.27	A	C
ATOM	1769	CB	GLU	A	353	-4.131	71.177	44.363	1.00	53.88	A	C
ATOM	1770	CG	GLU	A	353	-5.636	70.993	44.533	1.00	60.04	A	C
ATOM	1771	CD	GLU	A	353	-6.446	71.598	43.397	1.00	64.09	A	C
ATOM	1772	OE1	GLU	A	353	-6.082	72.700	42.921	1.00	64.63	A	O
ATOM	1773	OE2	GLU	A	353	-7.457	70.975	42.991	1.00	65.02	A	O
ATOM	1774	C	GLU	A	353	-2.088	70.989	42.969	1.00	49.88	A	C
ATOM	1775	O	GLU	A	353	-1.838	71.970	42.268	1.00	50.18	A	O
ATOM	1776	N	GLY	A	354	-1.154	70.319	43.635	1.00	47.30	A	N
ATOM	1777	CA	GLY	A	354	0.238	70.709	43.529	1.00	47.27	A	C
ATOM	1778	C	GLY	A	354	0.764	70.481	42.123	1.00	46.09	A	C
ATOM	1779	O	GLY	A	354	1.525	71.292	41.594	1.00	46.49	A	O
ATOM	1780	N	ALA	A	355	0.360	69.367	41.523	1.00	45.69	A	N
ATOM	1781	CA	ALA	A	355	0.764	69.018	40.164	1.00	45.85	A	C
ATOM	1782	CB	ALA	A	355	0.304	67.604	39.841	1.00	43.96	A	C
ATOM	1783	C	ALA	A	355	0.115	70.011	39.194	1.00	45.34	A	C
ATOM	1784	O	ALA	A	355	0.774	70.582	38.318	1.00	43.69	A	O
ATOM	1785	N	ARG	A	356	-1.188	70.210	39.374	1.00	44.80	A	N
ATOM	1786	CA	ARG	A	356	-1.964	71.121	38.547	1.00	43.64	A	C
ATOM	1787	CB	ARG	A	356	-3.429	71.110	39.008	1.00	43.97	A	C
ATOM	1788	CG	ARG	A	356	-4.084	69.742	38.844	1.00	44.00	A	C
ATOM	1789	CD	ARG	A	356	-5.299	69.539	39.760	1.00	46.78	A	C
ATOM	1790	NE	ARG	A	356	-6.562	69.930	39.146	1.00	46.50	A	N
ATOM	1791	CZ	ARG	A	356	-7.545	69.088	38.835	1.00	48.09	A	C
ATOM	1792	NH1	ARG	A	356	-7.423	67.793	39.078	1.00	45.87	A	N
ATOM	1793	NH2	ARG	A	356	-8.660	69.545	38.276	1.00	47.73	A	N
ATOM	1794	C	ARG	A	356	-1.387	72.534	38.584	1.00	42.30	A	C
ATOM	1795	O	ARG	A	356	-1.404	73.242	37.579	1.00	42.77	A	O
ATOM	1796	N	ASP	A	357	-0.850	72.938	39.728	1.00	39.68	A	N
ATOM	1797	CA	ASP	A	357	-0.273	74.267	39.836	1.00	41.20	A	C
ATOM	1798	CB	ASP	A	357	-0.047	74.645	41.305	1.00	45.03	A	C
ATOM	1799	CG	ASP	A	357	0.628	76.002	41.454	1.00	45.48	A	C
ATOM	1800	OD1	ASP	A	357	-0.080	77.030	41.454	1.00	49.20	A	O
ATOM	1801	OD2	ASP	A	357	1.872	76.046	41.544	1.00	46.68	A	O
ATOM	1802	C	ASP	A	357	1.054	74.381	39.081	1.00	41.64	A	C
ATOM	1803	O	ASP	A	357	1.326	75.406	38.448	1.00	41.73	A	O
ATOM	1804	N	LEU	A	358	1.888	73.343	39.153	1.00	41.39	A	N
ATOM	1805	CA	LEU	A	358	3.179	73.381	38.461	1.00	40.21	A	C
ATOM	1806	CB	LEU	A	358	4.060	72.189	38.858	1.00	40.82	A	C
ATOM	1807	CG	LEU	A	358	5.351	71.990	38.038	1.00	39.19	A	C
ATOM	1808	CD1	LEU	A	358	6.262	73.211	38.156	1.00	35.41	A	C
ATOM	1809	CD2	LEU	A	358	6.082	70.757	38.534	1.00	35.10	A	C
ATOM	1810	C	LEU	A	358	2.989	73.376	36.949	1.00	38.71	A	C
ATOM	1811	O	LEU	A	358	3.548	74.210	36.240	1.00	36.97	A	O
ATOM	1812	N	ILE	A	359	2.205	72.425	36.463	1.00	37.63	A	N
ATOM	1813	CA	ILE	A	359	1.958	72.318	35.036	1.00	37.27	A	C
ATOM	1814	CB	ILE	A	359	1.024	71.129	34.739	1.00	35.58	A	C
ATOM	1815	CG2	ILE	A	359	0.616	71.125	33.257	1.00	33.52	A	C
ATOM	1816	CG1	ILE	A	359	1.740	69.822	35.123	1.00	33.71	A	C
ATOM	1817	CD1	ILE	A	359	0.904	68.556	34.965	1.00	27.32	A	C
ATOM	1818	C	ILE	A	359	1.367	73.619	34.490	1.00	39.28	A	C
ATOM	1819	O	ILE	A	359	1.756	74.080	33.419	1.00	40.17	A	O
ATOM	1820	N	SER	A	360	0.448	74.219	35.243	1.00	39.65	A	N
ATOM	1821	CA	SER	A	360	-0.178	75.468	34.828	1.00	39.78	A	C
ATOM	1822	CB	SER	A	360	-1.326	75.824	35.774	1.00	38.05	A	C
ATOM	1823	OG	SER	A	360	-2.421	74.949	35.570	1.00	41.59	A	O
ATOM	1824	C	SER	A	360	0.803	76.634	34.732	1.00	38.08	A	C
ATOM	1825	O	SER	A	360	0.648	77.505	33.881	1.00	37.97	A	O
ATOM	1826	N	ARG	A	361	1.809	76.655	35.600	1.00	37.99	A	N
ATOM	1827	CA	ARG	A	361	2.809	77.722	35.568	1.00	38.96	A	C
ATOM	1828	CB	ARG	A	361	3.667	77.702	36.834	1.00	42.54	A	C
ATOM	1829	CG	ARG	A	361	2.988	78.154	38.121	1.00	50.26	A	C
ATOM	1830	CD	ARG	A	361	3.971	78.022	39.287	1.00	54.77	A	C

ATOM	1831	NE	ARG	A	361	3.358	78.286	40.586	1.00	60.68	A	N
ATOM	1832	CZ	ARG	A	361	2.987	79.490	41.010	1.00	63.56	A	C
ATOM	1833	NH1	ARG	A	361	2.435	79.631	42.211	1.00	65.68	A	N
ATOM	1834	NH2	ARG	A	361	3.171	80.554	40.238	1.00	63.46	A	N
ATOM	1835	C	ARG	A	361	3.745	77.560	34.371	1.00	36.65	A	C
ATOM	1836	O	ARG	A	361	4.273	78.537	33.838	1.00	34.66	A	O
ATOM	1837	N	LEU	A	362	3.956	76.314	33.966	1.00	34.75	A	N
ATOM	1838	CA	LEU	A	362	4.865	76.004	32.871	1.00	33.58	A	C
ATOM	1839	CB	LEU	A	362	5.370	74.563	33.019	1.00	33.55	A	C
ATOM	1840	CG	LEU	A	362	6.321	74.331	34.198	1.00	33.17	A	C
ATOM	1841	CD1	LEU	A	362	6.561	72.852	34.402	1.00	32.66	A	C
ATOM	1842	CD2	LEU	A	362	7.624	75.058	33.936	1.00	28.23	A	C
ATOM	1843	C	LEU	A	362	4.275	76.199	31.479	1.00	32.52	A	C
ATOM	1844	O	LEU	A	362	4.965	76.657	30.580	1.00	33.69	A	O
ATOM	1845	N	LEU	A	363	3.010	75.848	31.302	1.00	29.78	A	N
ATOM	1846	CA	LEU	A	363	2.369	75.985	29.997	1.00	33.86	A	C
ATOM	1847	CB	LEU	A	363	1.323	74.870	29.814	1.00	29.15	A	C
ATOM	1848	CG	LEU	A	363	1.817	73.401	29.868	1.00	31.05	A	C
ATOM	1849	CD1	LEU	A	363	0.631	72.468	29.746	1.00	24.51	A	C
ATOM	1850	CD2	LEU	A	363	2.837	73.123	28.748	1.00	24.89	A	C
ATOM	1851	C	LEU	A	363	1.726	77.371	29.798	1.00	34.25	A	C
ATOM	1852	O	LEU	A	363	0.508	77.505	29.740	1.00	36.86	A	O
ATOM	1853	N	LYS	A	364	2.565	78.396	29.710	1.00	38.02	A	N
ATOM	1854	CA	LYS	A	364	2.117	79.773	29.510	1.00	39.26	A	C
ATOM	1855	CB	LYS	A	364	2.907	80.735	30.407	1.00	40.63	A	C
ATOM	1856	CG	LYS	A	364	2.650	80.605	31.901	1.00	42.73	A	C
ATOM	1857	CD	LYS	A	364	1.227	81.004	32.237	1.00	45.77	A	C
ATOM	1858	CE	LYS	A	364	1.046	81.228	33.725	1.00	50.52	A	C
ATOM	1859	NZ	LYS	A	364	-0.323	81.742	34.024	1.00	54.71	A	N
ATOM	1860	C	LYS	A	364	2.372	80.145	28.057	1.00	39.30	A	C
ATOM	1861	O	LYS	A	364	3.496	79.997	27.569	1.00	38.57	A	O
ATOM	1862	N	HIS	A	365	1.335	80.616	27.368	1.00	39.57	A	N
ATOM	1863	CA	HIS	A	365	1.476	81.020	25.970	1.00	40.20	A	C
ATOM	1864	CB	HIS	A	365	0.187	81.659	25.451	1.00	40.44	A	C
ATOM	1865	CG	HIS	A	365	0.276	82.111	24.027	1.00	37.64	A	C
ATOM	1866	CD2	HIS	A	365	0.827	83.219	23.477	1.00	40.32	A	C
ATOM	1867	ND1	HIS	A	365	-0.179	81.349	22.974	1.00	38.59	A	N
ATOM	1868	CE1	HIS	A	365	0.088	81.963	21.836	1.00	36.60	A	C
ATOM	1869	NE2	HIS	A	365	0.699	83.101	22.113	1.00	41.15	A	N
ATOM	1870	C	HIS	A	365	2.606	82.031	25.839	1.00	40.73	A	C
ATOM	1871	O	HIS	A	365	3.430	81.948	24.925	1.00	41.73	A	O
ATOM	1872	N	ASN	A	366	2.637	82.997	26.753	1.00	42.45	A	N
ATOM	1873	CA	ASN	A	366	3.681	84.024	26.737	1.00	44.24	A	C
ATOM	1874	CB	ASN	A	366	3.183	85.272	27.477	1.00	44.55	A	C
ATOM	1875	CG	ASN	A	366	4.149	86.454	27.384	1.00	47.76	A	C
ATOM	1876	OD1	ASN	A	366	3.772	87.591	27.682	1.00	51.08	A	O
ATOM	1877	ND2	ASN	A	366	5.388	86.194	26.985	1.00	43.49	A	N
ATOM	1878	C	ASN	A	366	4.922	83.443	27.415	1.00	42.19	A	C
ATOM	1879	O	ASN	A	366	4.885	83.105	28.594	1.00	39.81	A	O
ATOM	1880	N	PRO	A	367	6.036	83.321	26.668	1.00	44.23	A	N
ATOM	1881	CD	PRO	A	367	6.151	83.761	25.267	1.00	43.04	A	C
ATOM	1882	CA	PRO	A	367	7.319	82.778	27.145	1.00	45.24	A	C
ATOM	1883	CB	PRO	A	367	8.252	82.989	25.953	1.00	44.30	A	C
ATOM	1884	CG	PRO	A	367	7.320	82.944	24.778	1.00	45.18	A	C
ATOM	1885	C	PRO	A	367	7.851	83.444	28.413	1.00	47.56	A	C
ATOM	1886	O	PRO	A	367	8.370	82.764	29.312	1.00	46.80	A	O
ATOM	1887	N	SER	A	368	7.716	84.770	28.470	1.00	47.18	A	N
ATOM	1888	CA	SER	A	368	8.162	85.579	29.607	1.00	47.72	A	C
ATOM	1889	CB	SER	A	368	7.926	87.076	29.334	1.00	48.23	A	C
ATOM	1890	OG	SER	A	368	8.681	87.537	28.227	1.00	51.49	A	O
ATOM	1891	C	SER	A	368	7.447	85.211	30.897	1.00	46.18	A	C
ATOM	1892	O	SER	A	368	7.988	85.406	31.989	1.00	48.13	A	O
ATOM	1893	N	GLN	A	369	6.228	84.699	30.787	1.00	45.87	A	N
ATOM	1894	CA	GLN	A	369	5.481	84.329	31.984	1.00	47.80	A	C
ATOM	1895	CB	GLN	A	369	3.973	84.295	31.697	1.00	51.34	A	C
ATOM	1896	CG	GLN	A	369	3.343	85.642	31.358	1.00	53.45	A	C
ATOM	1897	CD	GLN	A	369	1.840	85.530	31.120	1.00	57.46	A	C
ATOM	1898	OE1	GLN	A	369	1.061	85.287	32.048	1.00	60.02	A	O
ATOM	1899	NE2	GLN	A	369	1.430	85.698	29.872	1.00	58.61	A	N
ATOM	1900	C	GLN	A	369	5.916	82.983	32.561	1.00	47.67	A	C
ATOM	1901	O	GLN	A	369	5.606	82.668	33.715	1.00	46.25	A	O
ATOM	1902	N	ARG	A	370	6.628	82.188	31.765	1.00	46.58	A	N

ATOM	1903	CA	ARG	A	370	7.095	80.881	32.229	1.00	47.27	A	C
ATOM	1904	CB	ARG	A	370	7.596	80.040	31.042	1.00	43.84	A	C
ATOM	1905	CG	ARG	A	370	6.520	79.778	29.989	1.00	41.08	A	C
ATOM	1906	CD	ARG	A	370	7.094	79.136	28.732	1.00	42.55	A	C
ATOM	1907	NE	ARG	A	370	6.191	79.264	27.585	1.00	38.83	A	N
ATOM	1908	CZ	ARG	A	370	6.563	79.083	26.324	1.00	36.60	A	C
ATOM	1909	NH1	ARG	A	370	7.816	78.757	26.039	1.00	35.02	A	N
ATOM	1910	NH2	ARG	A	370	5.692	79.264	25.343	1.00	37.82	A	N
ATOM	1911	C	ARG	A	370	8.209	81.119	33.247	1.00	47.29	A	C
ATOM	1912	O	ARG	A	370	8.995	82.057	33.102	1.00	48.42	A	O
ATOM	1913	N	PRO	A	371	8.284	80.277	34.296	1.00	47.54	A	N
ATOM	1914	CD	PRO	A	371	7.383	79.135	34.552	1.00	46.07	A	C
ATOM	1915	CA	PRO	A	371	9.291	80.382	35.359	1.00	46.72	A	C
ATOM	1916	CB	PRO	A	371	8.772	79.410	36.415	1.00	45.48	A	C
ATOM	1917	CG	PRO	A	371	8.160	78.338	35.581	1.00	47.78	A	C
ATOM	1918	C	PRO	A	371	10.734	80.076	34.980	1.00	47.35	A	C
ATOM	1919	O	PRO	A	371	11.026	79.618	33.877	1.00	47.37	A	O
ATOM	1920	N	MET	A	372	11.642	80.357	35.911	1.00	48.69	A	N
ATOM	1921	CA	MET	A	372	13.055	80.067	35.713	1.00	47.91	A	C
ATOM	1922	CB	MET	A	372	13.923	80.961	36.598	1.00	51.73	A	C
ATOM	1923	CG	MET	A	372	13.788	82.444	36.324	1.00	56.54	A	C
ATOM	1924	SD	MET	A	372	14.948	83.405	37.339	1.00	60.67	A	S
ATOM	1925	CE	MET	A	372	16.321	83.556	36.190	1.00	59.45	A	C
ATOM	1926	C	MET	A	372	13.178	78.618	36.164	1.00	45.14	A	C
ATOM	1927	O	MET	A	372	12.344	78.139	36.929	1.00	44.11	A	O
ATOM	1928	N	LEU	A	373	14.204	77.917	35.703	1.00	44.75	A	N
ATOM	1929	CA	LEU	A	373	14.354	76.522	36.086	1.00	44.46	A	C
ATOM	1930	CB	LEU	A	373	15.526	75.893	35.325	1.00	42.40	A	C
ATOM	1931	CG	LEU	A	373	15.209	75.530	33.861	1.00	41.97	A	C
ATOM	1932	CD1	LEU	A	373	16.493	75.194	33.117	1.00	37.82	A	C
ATOM	1933	CD2	LEU	A	373	14.223	74.352	33.808	1.00	38.88	A	C
ATOM	1934	C	LEU	A	373	14.507	76.353	37.597	1.00	44.43	A	C
ATOM	1935	O	LEU	A	373	14.051	75.364	38.164	1.00	43.69	A	O
ATOM	1936	N	ALA	A	374	15.121	77.336	38.249	1.00	47.31	A	N
ATOM	1937	CA	ALA	A	374	15.310	77.289	39.699	1.00	48.80	A	C
ATOM	1938	CB	ALA	A	374	16.126	78.496	40.152	1.00	49.01	A	C
ATOM	1939	C	ALA	A	374	13.967	77.239	40.446	1.00	49.34	A	C
ATOM	1940	O	ALA	A	374	13.825	76.527	41.444	1.00	50.65	A	O
ATOM	1941	N	GLU	A	375	12.981	77.986	39.960	1.00	50.02	A	N
ATOM	1942	CA	GLU	A	375	11.662	78.006	40.582	1.00	50.79	A	C
ATOM	1943	CB	GLU	A	375	10.785	79.070	39.925	1.00	53.29	A	C
ATOM	1944	CG	GLU	A	375	11.341	80.477	39.993	1.00	58.36	A	C
ATOM	1945	CD	GLU	A	375	10.491	81.460	39.207	1.00	60.16	A	C
ATOM	1946	OE1	GLU	A	375	9.294	81.606	39.540	1.00	62.91	A	O
ATOM	1947	OE2	GLU	A	375	11.015	82.078	38.255	1.00	59.36	A	O
ATOM	1948	C	GLU	A	375	10.954	76.653	40.485	1.00	50.97	A	C
ATOM	1949	O	GLU	A	375	10.032	76.373	41.253	1.00	50.08	A	O
ATOM	1950	N	VAL	A	376	11.363	75.826	39.526	1.00	50.81	A	N
ATOM	1951	CA	VAL	A	376	10.765	74.502	39.358	1.00	50.86	A	C
ATOM	1952	CB	VAL	A	376	10.995	73.942	37.927	1.00	51.95	A	C
ATOM	1953	CG1	VAL	A	376	10.460	72.511	37.836	1.00	49.77	A	C
ATOM	1954	CG2	VAL	A	376	10.306	74.834	36.895	1.00	50.95	A	C
ATOM	1955	C	VAL	A	376	11.379	73.524	40.360	1.00	50.64	A	C
ATOM	1956	O	VAL	A	376	10.682	72.682	40.928	1.00	51.15	A	O
ATOM	1957	N	LEU	A	377	12.687	73.642	40.564	1.00	50.28	A	N
ATOM	1958	CA	LEU	A	377	13.413	72.782	41.492	1.00	52.39	A	C
ATOM	1959	CB	LEU	A	377	14.921	72.951	41.294	1.00	50.30	A	C
ATOM	1960	CG	LEU	A	377	15.497	72.434	39.973	1.00	49.77	A	C
ATOM	1961	CD1	LEU	A	377	16.942	72.875	39.830	1.00	47.65	A	C
ATOM	1962	CD2	LEU	A	377	15.393	70.919	39.911	1.00	48.67	A	C
ATOM	1963	C	LEU	A	377	13.054	73.091	42.944	1.00	54.42	A	C
ATOM	1964	O	LEU	A	377	13.302	72.283	43.841	1.00	55.25	A	O
ATOM	1965	N	GLU	A	378	12.467	74.263	43.169	1.00	55.92	A	N
ATOM	1966	CA	GLU	A	378	12.075	74.676	44.510	1.00	56.51	A	C
ATOM	1967	CB	GLU	A	378	12.597	76.079	44.791	1.00	57.88	A	C
ATOM	1968	CG	GLU	A	378	14.102	76.137	44.929	1.00	61.78	A	C
ATOM	1969	CD	GLU	A	378	14.631	77.545	44.819	1.00	65.68	A	C
ATOM	1970	OE1	GLU	A	378	15.846	77.741	45.039	1.00	68.31	A	O
ATOM	1971	OE2	GLU	A	378	13.834	78.456	44.502	1.00	67.56	A	O
ATOM	1972	C	GLU	A	378	10.569	74.639	44.721	1.00	55.69	A	C
ATOM	1973	O	GLU	A	378	10.081	75.016	45.784	1.00	57.50	A	O
ATOM	1974	N	HIS	A	379	9.832	74.183	43.715	1.00	52.52	A	N

ATOM	1975	CA	HIS	A	379	8.381	74.103	43.824	1.00	50.30	A	C
ATOM	1976	CB	HIS	A	379	7.773	73.684	42.484	1.00	46.98	A	C
ATOM	1977	CG	HIS	A	379	6.276	73.759	42.441	1.00	45.89	A	C
ATOM	1978	CD2	HIS	A	379	5.446	74.721	41.969	1.00	43.25	A	C
ATOM	1979	ND1	HIS	A	379	5.463	72.753	42.922	1.00	44.60	A	N
ATOM	1980	CE1	HIS	A	379	4.197	73.090	42.746	1.00	42.55	A	C
ATOM	1981	NE2	HIS	A	379	4.159	74.279	42.170	1.00	45.42	A	N
ATOM	1982	C	HIS	A	379	8.002	73.108	44.918	1.00	51.08	A	C
ATOM	1983	O	HIS	A	379	8.526	71.992	44.975	1.00	50.77	A	O
ATOM	1984	N	PRO	A	380	7.076	73.506	45.804	1.00	52.09	A	N
ATOM	1985	CD	PRO	A	380	6.283	74.747	45.721	1.00	52.19	A	C
ATOM	1986	CA	PRO	A	380	6.612	72.669	46.913	1.00	50.97	A	C
ATOM	1987	CB	PRO	A	380	5.502	73.519	47.546	1.00	51.57	A	C
ATOM	1988	CG	PRO	A	380	5.003	74.343	46.401	1.00	53.46	A	C
ATOM	1989	C	PRO	A	380	6.146	71.257	46.549	1.00	49.66	A	C
ATOM	1990	O	PRO	A	380	6.253	70.340	47.361	1.00	48.94	A	O
ATOM	1991	N	TRP	A	381	5.626	71.074	45.341	1.00	47.98	A	N
ATOM	1992	CA	TRP	A	381	5.169	69.751	44.936	1.00	46.47	A	C
ATOM	1993	CB	TRP	A	381	4.188	69.854	43.774	1.00	45.54	A	C
ATOM	1994	CG	TRP	A	381	3.631	68.527	43.346	1.00	40.93	A	C
ATOM	1995	CD2	TRP	A	381	4.049	67.743	42.222	1.00	40.08	A	C
ATOM	1996	CE2	TRP	A	381	3.226	66.595	42.185	1.00	38.42	A	C
ATOM	1997	CE3	TRP	A	381	5.036	67.900	41.238	1.00	40.44	A	C
ATOM	1998	CD1	TRP	A	381	2.606	67.840	43.932	1.00	41.28	A	C
ATOM	1999	NE1	TRP	A	381	2.356	66.681	43.240	1.00	40.02	A	N
ATOM	2000	CZ2	TRP	A	381	3.359	65.605	41.200	1.00	38.16	A	C
ATOM	2001	CZ3	TRP	A	381	5.167	66.914	40.257	1.00	39.27	A	C
ATOM	2002	CH2	TRP	A	381	4.332	65.783	40.248	1.00	35.86	A	C
ATOM	2003	C	TRP	A	381	6.362	68.898	44.516	1.00	46.87	A	C
ATOM	2004	O	TRP	A	381	6.373	67.683	44.718	1.00	46.53	A	O
ATOM	2005	N	ILE	A	382	7.362	69.539	43.917	1.00	48.95	A	N
ATOM	2006	CA	ILE	A	382	8.566	68.835	43.485	1.00	50.95	A	C
ATOM	2007	CB	ILE	A	382	9.489	69.749	42.634	1.00	49.30	A	C
ATOM	2008	CG2	ILE	A	382	10.821	69.053	42.398	1.00	48.74	A	C
ATOM	2009	CG1	ILE	A	382	8.822	70.098	41.294	1.00	49.61	A	C
ATOM	2010	CD1	ILE	A	382	8.619	68.907	40.358	1.00	42.81	A	C
ATOM	2011	C	ILE	A	382	9.341	68.384	44.725	1.00	53.01	A	C
ATOM	2012	O	ILE	A	382	9.651	67.203	44.889	1.00	51.75	A	O
ATOM	2013	N	THR	A	383	9.643	69.340	45.596	1.00	56.54	A	N
ATOM	2014	CA	THR	A	383	10.384	69.069	46.827	1.00	60.42	A	C
ATOM	2015	CB	THR	A	383	10.615	70.364	47.629	1.00	60.63	A	C
ATOM	2016	OG1	THR	A	383	11.390	71.279	46.844	1.00	62.34	A	O
ATOM	2017	CG2	THR	A	383	11.360	70.067	48.923	1.00	64.67	A	C
ATOM	2018	C	THR	A	383	9.667	68.070	47.726	1.00	61.26	A	C
ATOM	2019	O	THR	A	383	10.303	67.355	48.501	1.00	62.87	A	O
ATOM	2020	N	ALA	A	384	8.346	68.010	47.609	1.00	61.81	A	N
ATOM	2021	CA	ALA	A	384	7.554	67.104	48.427	1.00	62.66	A	C
ATOM	2022	CB	ALA	A	384	6.140	67.656	48.585	1.00	63.07	A	C
ATOM	2023	C	ALA	A	384	7.493	65.668	47.909	1.00	63.07	A	C
ATOM	2024	O	ALA	A	384	7.337	64.735	48.695	1.00	63.72	A	O
ATOM	2025	N	ASN	A	385	7.612	65.482	46.597	1.00	62.18	A	N
ATOM	2026	CA	ASN	A	385	7.550	64.140	46.025	1.00	62.42	A	C
ATOM	2027	CB	ASN	A	385	6.466	64.083	44.946	1.00	61.14	A	C
ATOM	2028	CG	ASN	A	385	5.078	64.372	45.491	1.00	60.33	A	C
ATOM	2029	OD1	ASN	A	385	4.427	63.499	46.065	1.00	57.45	A	O
ATOM	2030	ND2	ASN	A	385	4.623	65.610	45.317	1.00	56.76	A	N
ATOM	2031	C	ASN	A	385	8.871	63.653	45.430	1.00	63.75	A	C
ATOM	2032	O	ASN	A	385	9.030	62.466	45.154	1.00	63.17	A	O
ATOM	2033	N	SER	A	386	9.814	64.565	45.234	1.00	66.08	A	N
ATOM	2034	CA	SER	A	386	11.103	64.211	44.651	1.00	69.04	A	C
ATOM	2035	CB	SER	A	386	11.731	65.441	43.990	1.00	70.22	A	C
ATOM	2036	OG	SER	A	386	13.032	65.159	43.503	1.00	70.59	A	O
ATOM	2037	C	SER	A	386	12.093	63.626	45.654	1.00	72.01	A	C
ATOM	2038	O	SER	A	386	12.098	63.989	46.833	1.00	73.11	A	O
ATOM	2039	N	SER	A	387	12.931	62.717	45.169	1.00	73.40	A	N
ATOM	2040	CA	SER	A	387	13.951	62.088	45.995	1.00	75.94	A	C
ATOM	2041	CB	SER	A	387	14.024	60.589	45.695	1.00	75.91	A	C
ATOM	2042	OG	SER	A	387	12.754	59.981	45.840	1.00	76.94	A	O
ATOM	2043	C	SER	A	387	15.284	62.751	45.650	1.00	77.73	A	C
ATOM	2044	O	SER	A	387	16.348	62.280	46.058	1.00	78.06	A	O
ATOM	2045	N	LYS	A	388	15.194	63.843	44.886	1.00	78.26	A	N
ATOM	2046	CA	LYS	A	388	16.339	64.635	44.428	1.00	79.08	A	C

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ATOM  2047  CB  LYS A 388      17.409  64.724  45.525  1.00 79.44      A     C
ATOM  2048  CG  LYS A 388      16.974  65.500  46.763  1.00 79.33      A     C
ATOM  2049  CD  LYS A 388      18.062  65.484  47.824  1.00 79.09      A     C
ATOM  2050  CE  LYS A 388      17.695  66.350  49.018  1.00 79.02      A     C
ATOM  2051  NZ  LYS A 388      17.530  67.782  48.641  1.00 78.19      A     N
ATOM  2052  C   LYS A 388      16.959  64.102  43.130  1.00 78.82      A     C
ATOM  2053  O   LYS A 388      16.481  63.074  42.619  1.00 78.44      A     O
ATOM  2054  OXT LYS A 388      17.916  64.723  42.618  1.00 79.61      A     O
ATOM  2056  PB AANP Z 379      15.037  57.738  17.969  0.50 47.69      Z     P
ATOM  2057  PB BANP Z 379      17.785  58.350  20.389  0.50 50.58      Z     P
ATOM  2058  O1BAANP Z 379      15.506  57.453  19.308  0.50 49.57      Z     O
ATOM  2059  O1BBANP Z 379      18.803  57.539  21.023  0.50 51.23      Z     O
ATOM  2060  O2BAANP Z 379      14.617  59.160  17.829  0.50 48.87      Z     O
ATOM  2061  O2BBANP Z 379      18.020  59.811  20.601  0.50 52.85      Z     O
ATOM  2062  O3BAANP Z 379      13.854  56.738  17.611  0.50 47.44      Z     O
ATOM  2063  O3BBANP Z 379      16.375  57.916  20.971  0.50 53.88      Z     O
ATOM  2064  PA AANP Z 379      17.533  56.644  17.115  0.50 51.30      Z     P
ATOM  2065  PA BANP Z 379      18.302  56.815  17.978  0.50 49.99      Z     P
ATOM  2066  O1AAANP Z 379      18.137  56.443  15.785  0.50 52.19      Z     O
ATOM  2067  O1ABANP Z 379      17.740  56.898  16.602  0.50 51.27      Z     O
ATOM  2068  O2AAANP Z 379      18.354  57.484  18.041  0.50 51.52      Z     O
ATOM  2069  O2ABANP Z 379      19.779  56.935  18.073  0.50 51.64      Z     O
ATOM  2070  O3AAANP Z 379      16.105  57.302  16.924  0.50 51.44      Z     O
ATOM  2071  O3ABANP Z 379      17.600  57.938  18.878  0.50 50.89      Z     O
ATOM  2072  O5*AANP Z 379      17.177  55.295  17.877  0.50 50.92      Z     O
ATOM  2073  O5*BANP Z 379      17.867  55.497  18.751  0.50 47.15      Z     O
ATOM  2074  C5*AANP Z 379      17.877  54.090  17.490  0.50 47.94      Z     C
ATOM  2075  C5*BANP Z 379      17.722  54.257  18.009  0.50 40.88      Z     C
ATOM  2076  C4*AANP Z 379      17.460  52.862  18.318  0.50 47.92      Z     C
ATOM  2077  C4*BANP Z 379      17.263  53.099  18.926  0.50 36.96      Z     C
ATOM  2078  O4*AANP Z 379      18.576  52.400  19.179  0.50 47.21      Z     O
ATOM  2079  O4*BANP Z 379      18.369  52.549  19.752  0.50 33.82      Z     O
ATOM  2080  C3*AANP Z 379      16.328  53.019  19.359  0.50 47.98      Z     C
ATOM  2081  C3*BANP Z 379      16.203  53.417  20.009  0.50 33.98      Z     C
ATOM  2082  O3*AANP Z 379      15.560  51.846  19.588  0.50 48.47      Z     O
ATOM  2083  O3*BANP Z 379      15.320  52.350  20.339  0.50 32.96      Z     O
ATOM  2084  C2*AANP Z 379      17.076  53.566  20.584  0.50 47.21      Z     C
ATOM  2085  C2*BANP Z 379      17.064  53.934  21.164  0.50 32.17      Z     C
ATOM  2086  O2*AANP Z 379      16.398  53.519  21.825  0.50 48.99      Z     O
ATOM  2087  O2*BANP Z 379      16.446  54.056  22.437  0.50 30.71      Z     O
ATOM  2088  C1*AANP Z 379      18.369  52.807  20.558  0.50 46.20      Z     C
ATOM  2089  C1*BANP Z 379      18.273  53.024  21.121  0.50 31.00      Z     C
ATOM  2090  N9 AANP Z 379      19.533  53.632  21.081  0.50 44.22      Z     N
ATOM  2091  N9 BANP Z 379      19.537  53.738  21.552  0.50 27.84      Z     N
ATOM  2092  C8 AANP Z 379      20.137  54.688  20.410  0.50 43.51      Z     C
ATOM  2093  C8 BANP Z 379      20.190  54.721  20.820  0.50 26.21      Z     C
ATOM  2094  N7 AANP Z 379      21.138  55.258  21.064  0.50 43.16      Z     N
ATOM  2095  N7 BANP Z 379      21.273  55.211  21.389  0.50 27.05      Z     N
ATOM  2096  C5 AANP Z 379      21.222  54.563  22.228  0.50 43.37      Z     C
ATOM  2097  C5 BANP Z 379      21.372  54.538  22.561  0.50 27.46      Z     C
ATOM  2098  C6 AANP Z 379      22.077  54.630  23.408  0.50 41.80      Z     C
ATOM  2099  C6 BANP Z 379      22.300  54.555  23.675  0.50 26.76      Z     C
ATOM  2100  N6 AANP Z 379      23.058  55.506  23.571  0.50 41.70      Z     N
ATOM  2101  N6 BANP Z 379      23.356  55.348  23.750  0.50 26.20      Z     N
ATOM  2102  N1 AANP Z 379      21.858  53.706  24.460  0.50 43.30      Z     N
ATOM  2103  N1 BANP Z 379      22.075  53.675  24.765  0.50 29.25      Z     N
ATOM  2104  C2 AANP Z 379      20.844  52.746  24.372  0.50 42.75      Z     C
ATOM  2105  C2 BANP Z 379      20.979  52.806  24.765  0.50 27.75      Z     C
ATOM  2106  N3 AANP Z 379      19.992  52.607  23.302  0.50 43.98      Z     N
ATOM  2107  N3 BANP Z 379      20.052  52.720  23.761  0.50 28.35      Z     N
ATOM  2108  C4 AANP Z 379      20.223  53.538  22.258  0.50 43.59      Z     C
ATOM  2109  C4 BANP Z 379      20.292  53.604  22.682  0.50 27.97      Z     C
ATOM  2110  P1  FRA Z 379      26.094  48.843  31.713  1.00 52.95      Z     P
ATOM  2111  O2  FRA Z 379      27.446  48.301  31.747  1.00 53.45      Z     O
ATOM  2112  O3  FRA Z 379      25.842  49.670  32.927  1.00 57.52      Z     O
ATOM  2113  O4  FRA Z 379      25.079  47.640  31.660  1.00 53.32      Z     O
ATOM  2114  O5  FRA Z 379      25.925  49.788  30.418  1.00 54.94      Z     O
TER   2115      FRAGZ   1                      Z
ATOM  2116  O   HOH W 379       0.331  67.542  23.164  1.00 33.20      W     O
ATOM  2117  O   HOH W 380      28.844  46.119  11.651  1.00 48.79      W     O
ATOM  2118  O   HOH W 381      23.007  73.689  19.317  1.00 39.02      W     O
ATOM  2119  O   HOH W 382      10.568  41.141  28.154  1.00 49.97      W     O
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ATOM	2120	O	HOH W 383	12.722	71.913	24.732	1.00	38.33	W	O
ATOM	2121	O	HOH W 384	27.119	63.991	29.594	1.00	34.78	W	O
ATOM	2122	O	HOH W 385	25.822	60.889	31.761	1.00	35.64	W	O
ATOM	2123	O	HOH W 386	12.649	51.436	29.438	1.00	30.54	W	O
ATOM	2124	O	HOH W 387	-1.136	77.886	32.084	1.00	58.06	W	O
ATOM	2125	O	HOH W 388	-5.994	68.177	27.794	1.00	32.43	W	O
ATOM	2126	O	HOH W 389	30.025	50.004	9.061	1.00	46.99	W	O
ATOM	2127	O	HOH W 390	-3.566	81.854	26.459	1.00	55.28	W	O
ATOM	2128	O	HOH W 391	30.646	47.521	34.093	1.00	60.01	W	O
ATOM	2129	O	HOH W 392	-1.097	85.911	26.783	1.00	47.89	W	O
ATOM	2130	O	HOH W 393	0.595	65.227	46.406	1.00	53.88	W	O
ATOM	2131	O	HOH W 394	6.207	71.002	50.031	1.00	52.47	W	O
ATOM	2132	O	HOH W 395	5.278	55.170	38.782	1.00	41.90	W	O
ATOM	2133	O	HOH W 396	-12.360	69.423	40.011	1.00	62.19	W	O
ATOM	2134	O	HOH W 397	10.584	80.817	23.752	1.00	42.95	W	O
ATOM	2135	O	HOH W 398	20.285	61.152	38.189	1.00	57.76	W	O
ATOM	2136	O	HOH W 399	38.138	63.320	28.926	1.00	63.01	W	O
ATOM	2137	O	HOH W 400	36.205	63.417	18.017	1.00	42.85	W	O
ATOM	2138	O	HOH W 401	10.940	46.826	29.244	1.00	66.42	W	O
ATOM	2139	O	HOH W 402	28.740	45.402	31.083	1.00	57.98	W	O
ATOM	2140	O	HOH W 403	16.667	51.609	23.943	1.00	49.28	W	O
ATOM	2141	O	HOH W 404	0.650	83.566	28.516	1.00	48.67	W	O
ATOM	2142	O	HOH W 405	23.052	81.277	32.597	1.00	79.68	W	O
ATOM	2143	O	HOH W 406	21.015	66.488	25.190	1.00	51.11	W	O
ATOM	2144	O	HOH W 407	29.555	78.569	17.681	1.00	72.97	W	O
ATOM	2145	O	HOH W 408	23.196	68.069	19.434	1.00	38.38	W	O
ATOM	2146	O	HOH W 409	-7.313	65.296	29.334	1.00	66.68	W	O
ATOM	2147	O	HOH W 410	24.377	54.450	33.733	1.00	39.04	W	O
ATOM	2148	O	HOH W 411	18.676	56.503	40.201	1.00	43.61	W	O
ATOM	2149	O	HOH W 412	19.799	63.234	10.818	1.00	60.37	W	O
ATOM	2150	O	HOH W 413	4.227	81.623	22.473	1.00	45.07	W	O
ATOM	2151	O	HOH W 414	35.586	63.256	25.029	1.00	58.40	W	O
ATOM	2152	O	HOH W 415	26.042	47.904	6.604	1.00	63.98	W	O
ATOM	2153	O	HOH W 416	0.125	61.540	20.664	1.00	58.49	W	O
ATOM	2154	O	HOH W 417	15.750	58.426	38.595	1.00	51.37	W	O
ATOM	2155	O	HOH W 418	8.114	48.760	24.263	1.00	66.46	W	O
ATOM	2156	O	HOH W 419	-13.534	60.538	36.389	1.00	56.48	W	O
ATOM	2157	O	HOH W 420	37.492	60.906	4.499	1.00	56.53	W	O
ATOM	2158	O	HOH W 421	11.597	49.198	40.125	1.00	55.46	W	O
ATOM	2159	O	HOH W 422	29.535	40.480	27.301	1.00	39.07	W	O
ATOM	2160	O	HOH W 423	-9.419	60.202	32.744	1.00	49.49	W	O
ATOM	2161	O	HOH W 424	-3.387	80.285	33.001	1.00	53.18	W	O
ATOM	2162	O	HOH W 425	22.854	68.702	38.913	1.00	56.31	W	O
ATOM	2163	O	HOH W 426	5.516	90.168	27.801	1.00	57.26	W	O
ATOM	2164	O	HOH W 427	42.341	62.424	13.295	1.00	70.57	W	O
ATOM	2165	O	HOH W 428	50.104	46.432	21.896	1.00	59.70	W	O
ATOM	2166	O	HOH W 429	19.133	50.530	8.236	1.00	38.20	W	O
ATOM	2167	O	HOH W 430	14.218	90.460	15.295	1.00	59.43	W	O
ATOM	2168	O	HOH W 431	20.996	76.724	18.128	1.00	68.02	W	O
ATOM	2169	O	HOH W 432	28.748	65.408	11.519	1.00	55.89	W	O
ATOM	2170	O	HOH W 433	33.109	52.617	3.045	1.00	66.13	W	O
ATOM	2171	O	HOH W 434	-0.097	51.530	27.181	1.00	62.48	W	O
ATOM	2172	O	HOH W 435	34.328	49.913	33.453	1.00	80.02	W	O
ATOM	2173	O	HOH W 436	16.321	46.597	36.609	1.00	55.74	W	O
ATOM	2174	O	HOH W 437	15.506	88.823	36.550	1.00	60.31	W	O
ATOM	2175	O	HOH W 438	-10.288	68.090	36.659	1.00	43.23	W	O
ATOM	2176	O	HOH W 439	35.236	49.316	7.956	1.00	47.01	W	O
ATOM	2177	O	HOH W 440	-2.382	64.267	14.669	1.00	54.31	W	O
ATOM	2178	O	HOH W 441	3.145	71.184	22.878	1.00	32.15	W	O
ATOM	2179	O	HOH W 442	13.920	51.205	25.014	1.00	47.83	W	O
ATOM	2180	O	HOH W 443	-0.162	59.596	37.808	1.00	46.99	W	O
ATOM	2181	O	HOH W 444	21.993	67.937	15.891	1.00	41.38	W	O
ATOM	2182	O	HOH W 445	18.406	49.826	26.693	1.00	48.92	W	O
ATOM	2183	O	HOH W 446	27.317	49.713	35.324	1.00	50.93	W	O
ATOM	2184	O	HOH W 447	32.044	55.554	32.480	1.00	59.20	W	O
ATOM	2185	O	HOH W 448	15.585	66.847	22.965	1.00	66.60	W	O
ATOM	2186	O	HOH W 449	28.577	85.371	20.089	1.00	61.69	W	O
ATOM	2187	O	HOH W 450	19.255	74.406	43.569	1.00	78.23	W	O
ATOM	2188	O	HOH W 451	46.877	44.566	20.648	1.00	63.82	W	O
ATOM	2189	O	HOH W 452	18.724	77.353	37.945	1.00	74.74	W	O
ATOM	2190	O	HOH W 453	32.145	68.599	9.155	1.00	80.54	W	O
ATOM	2191	O	HOH W 454	4.355	81.219	35.183	1.00	34.92	W	O

ATOM	2192	O	HOH W 455	25.635	56.901	34.614	1.00	47.34	W	O		
ATOM	2193	O	HOH W 456	42.338	49.434	11.100	1.00	72.43	W	O		
ATOM	2194	O	HOH W 457	-2.051	65.103	18.494	1.00	39.83	W	O		
ATOM	2195	O	HOH W 458	-9.591	72.598	44.168	1.00	64.69	W	O		
ATOM	2196	O	HOH W 459	20.373	46.614	27.914	1.00	38.68	W	O		
ATOM	2197	O	HOH W 460	0.659	55.516	18.515	1.00	58.39	W	O		
ATOM	2198	O	HOH W 461	21.076	80.510	26.713	1.00	61.17	W	O		
ATOM	2199	O	HOH W 462	32.155	47.583	8.094	1.00	70.56	W	O		
ATOM	2200	O	HOH W 463	4.044	58.878	44.996	1.00	51.08	W	O		
ATOM	2201	O	HOH W 464	41.005	53.749	30.770	1.00	75.59	W	O		
ATOM	2202	O	HOH W 465	26.371	63.533	-4.679	1.00	74.46	W	O		
ATOM	2203	O	HOH W 466	18.683	73.320	26.848	1.00	53.79	W	O		
ATOM	2204	O	HOH W 467	31.520	71.009	32.011	1.00	56.96	W	O		
ATOM	2205	O	HOH W 468	17.101	44.021	28.295	1.00	65.42	W	O		
ATOM	2206	O	HOH W 469	39.280	50.487	10.873	1.00	71.08	W	O		
ATOM	2207	O	HOH W 470	37.290	42.352	23.513	1.00	70.13	W	O		
ATOM	2208	O	HOH W 471	5.578	77.441	49.897	1.00	69.56	W	O		
ATOM	2209	O	HOH W 472	7.437	83.010	37.688	1.00	69.84	W	O		
ATOM	2210	O	HOH W 473	26.352	64.806	24.911	1.00	54.06	W	O		
ATOM	2211	O	HOH W 474	11.127	50.403	42.491	1.00	74.19	W	O		
ATOM	2212	O	HOH W 475	13.078	66.605	47.781	1.00	64.41	W	O		
ATOM	2213	O	HOH W 476	33.069	47.485	4.075	1.00	73.62	W	O		
ATOM	2214	O	HOH W 477	16.310	47.636	28.660	1.00	60.28	W	O		
ATOM	2215	O	HOH W 478	10.526	56.684	48.949	1.00	65.54	W	O		
ATOM	2216	O	HOH W 479	8.120	87.653	17.142	1.00	54.25	W	O		
ATOM	2217	O	HOH W 480	8.395	84.399	35.638	1.00	53.58	W	O		
ATOM	2218	O	HOH W 481	37.470	55.653	9.464	1.00	46.07	W	O		
ATOM	2219	O	HOH W 482	26.702	61.295	39.749	1.00	63.14	W	O		
ATOM	2220	O	HOH W 483	45.743	51.322	22.505	1.00	64.82	W	O		
ATOM	2221	O	HOH W 484	26.243	53.676	32.375	1.00	76.35	W	O		
ATOM	2222	O	HOH W 485	28.613	53.324	28.097	1.00	38.88	W	O		
ATOM	2223	O	HOH W 486	4.244	65.989	13.927	1.00	36.47	W	O		
ATOM	2224	O	HOH W 487	24.103	54.829	31.073	1.00	48.23	W	O		
ATOM	2225	O	HOH W 488	16.440	64.104	14.517	1.00	46.59	W	O		
ATOM	2226	O	HOH W 489	37.058	53.211	10.107	1.00	41.19	W	O		
ATOM	2227	O	HOH W 490	1.626	58.930	43.465	1.00	56.15	W	O		
ATOM	2228	O	HOH W 491	5.404	80.824	37.937	1.00	49.30	W	O		
ATOM	2229	O	HOH W 492	3.696	83.191	19.871	1.00	55.84	W	O		
ATOM	2230	O	HOH W 493	9.216	69.339	23.781	1.00	49.12	W	O		
ATOM	2231	O	HOH W 494	36.460	55.040	25.386	1.00	61.90	W	O		
ATOM	2232	O	HOH W 495	29.035	64.618	25.993	1.00	44.19	W	O		
ATOM	2233	O	HOH W 496	-1.211	81.253	28.481	1.00	49.42	W	O		
ATOM	2234	O	HOH W 497	-13.349	74.056	40.995	1.00	57.64	W	O		
ATOM	2235	O	HOH W 498	22.952	75.394	20.894	1.00	54.51	W	O		
ATOM	2236	O	HOH W 499	8.061	54.650	41.586	1.00	49.70	W	O		
ATOM	2237	O	HOH W 500	-4.078	73.918	41.599	1.00	51.57	W	O		
ATOM	2238	O	HOH W 501	26.284	56.747	2.127	1.00	52.08	W	O		
ATOM	2239	O	HOH W 502	30.005	48.619	30.666	1.00	72.19	W	O		
ATOM	2240	O	HOH W 503	20.159	65.366	13.420	1.00	51.24	W	O		
ATOM	2241	O	HOH W 504	-5.361	63.850	28.736	1.00	60.73	W	O		
ATOM	2242	O	HOH W 505	26.955	52.505	30.145	1.00	52.17	W	O		
ATOM	2243	O	HOH W 506	0.745	55.925	28.349	1.00	47.50	W	O		
ATOM	2244	O	HOH W 507	13.465	63.276	17.023	1.00	63.56	W	O		
ATOM	2245	O	HOH W 508	-0.920	64.629	40.572	1.00	40.57	W	O		
ATOM	2246	O	HOH W 509	-8.382	72.769	39.661	1.00	58.85	W	O		
ATOM	2247	O	HOH W 510	19.488	70.756	41.864	1.00	49.15	W	O		
ATOM	2248	O	HOH W 511	14.101	54.714	36.057	1.00	57.27	W	O		
ATOM	2249	O	HOH W 512	31.885	61.378	38.523	1.00	62.27	W	O		
ATOM	2250	O	HOH W 513	35.755	51.839	8.257	1.00	47.13	W	O		
ATOM	2251	O	HOH W 514	17.069	82.457	25.470	1.00	55.98	W	O		
ATOM	2252	O	HOH W 515	-4.640	64.734	26.208	1.00	35.90	W	O		
ATOM	2253	O	HOH W 516	28.342	79.720	28.289	1.00	51.97	W	O		
ATOM	2254	O	HOH W 517	28.930	63.693	33.886	1.00	47.21	W	O		
ATOM	2255	O	HOH W 518	14.019	51.336	17.356	1.00	74.59	W	O		
ATOM	2256	O	HOH W 519	16.446	79.651	42.696	1.00	66.23	W	O		
ATOM	2257	O	HOH W 520	32.520	63.699	25.738	1.00	57.23	W	O		
ATOM	2258	O	HOH W 521	-11.168	62.126	35.907	1.00	65.36	W	O		
ATOM	2259	O	HOH W 522	13.702	76.196	48.300	1.00	61.59	W	O		
ATOM	2260	O	HOH W 523	1.241	58.718	25.331	1.00	64.44	W	O		
ATOM	2261	O	HOH W 524	14.477	78.178	21.588	1.00	64.83	W	O		
ATOM	2262	O	HOH W 525	12.372	54.887	20.646	1.00	60.88	W	O		
ATOM	2263	O	HOH W 526	7.266	74.256	14.263	1.00	39.73	W	O		

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ATOM   2264  O    HOH W 527      20.091  44.006  35.105  1.00 50.82      W    O
ATOM   2265  O    HOH W 528       1.165  69.375  46.475  1.00 57.89      W    O
ATOM   2266  O    HOH W 529      19.142  46.127  35.660  1.00 45.19      W    O
ATOM   2267  O    HOH W 530      42.086  55.304  19.791  1.00 71.79      W    O
ATOM   2268  O    HOH W 531      25.087  50.111  39.148  1.00 63.76      W    O
ATOM   2269  O    HOH W 532       5.318  61.373  18.508  1.00 62.59      W    O
ATOM   2270  O    HOH W 533      29.675  78.586  23.627  1.00 58.56      W    O
ATOM   2271  O    HOH W 534      19.557  76.701  12.869  1.00 68.72      W    O
ATOM   2272  O    HOH W 535      42.115  57.119  21.522  1.00 71.32      W    O
ATOM   2273  O    HOH W 536       0.634  77.003  19.831  1.00100.00      W    O
ATOM   2274  O    HOH W 537      19.709  88.994  42.992  1.00 58.23      W    O
ATOM   2275  O    HOH W 538      13.524  50.624  47.508  1.00 75.63      W    O
ATOM   2276  O    HOH W 539      11.617  86.001  30.094  1.00 68.80      W    O
ATOM   2277  O    HOH W 540      -7.680  59.135  43.088  1.00 61.92      W    O
TER    2278       HOH W 205                                              W
ATOM   2279  C1   FRA V 541      18.019  80.374  32.848  1.00 57.37      V    C
ATOM   2280  C2   FRA V 541      17.378  79.416  33.865  1.00 55.67      V    C
ATOM   2281  C3   FRA V 541      17.724  79.837  35.320  1.00 57.54      V    C
ATOM   2282  O4   FRA V 541      17.702  79.994  31.523  1.00 54.83      V    O
ATOM   2283  O5   FRA V 541      15.964  79.445  33.671  1.00 53.75      V    O
ATOM   2284  O6   FRA V 541      16.818  79.285  36.284  1.00 58.10      V    O
ATOM   2285  O    HOH V 542      21.116  58.251  20.758  1.00 34.64      V    O
TER    2286       HOH V   2                                              V
END
```

Table 2 – coordinates for the two molecules in the asymmetric unit of [T287] Aurora A (122-396) in complex with an inhibitor of formula II in space group $P2_1$

```
REMARK  [No title given]
REMARK  [No title given]
REMARK  [No title given]
REMARK Aurora complex with M535136.  Refined structure.  Solved by
REMARK molecular replacement using a partly refined aurora structure
REMARK from the trigonal crystal form.  Original MR model derived
REMARK from a PKA alignment.  Inhibitor occupies much of active site
REMARK cleft and usual interactions at adenine site.  Superposition
REMARK with PKA shows a very wide, open active site cleft.
REMARK coordinates from restrained individual B-factor refinement
REMARK refinement resolution: 500.0 - 2.1 A
REMARK starting r= 0.2306 free_r= 0.2716
REMARK final    r= 0.2256 free_r= 0.2677
REMARK B rmsd for bonded mainchain atoms=  1.521  target= 1.5
REMARK B rmsd for bonded sidechain atoms=  2.205  target= 2.0
REMARK B rmsd for angle mainchain atoms=  2.492  target= 2.0
REMARK B rmsd for angle sidechain atoms=  3.350  target= 2.5
REMARK rweight=  0.1000 (with wa= 3.00741)
REMARK target= mlf  steps= 30
REMARK sg= P2(1)a= 52.603 b= 88.421 c= 67.832 alpha=90 beta= 90.013 gamma= 90
REMARK parameter file 1  : MSI_CNX_TOPPAR:protein_rep.param
REMARK parameter file 2  : fra.par
REMARK parameter file 3  : MSI_CNX_TOPPAR:water_rep.param
REMARK molecular structure file: reb9.mtf
REMARK input coordinates: anneal_reb_1.pdb
REMARK reflection file= aurora-p21.cv
REMARK ncs= none
REMARK B-correction resolution: 6.0 - 2.1
REMARK initial B-factor correction applied to fobs :
REMARK    B11=   1.629 B22=  -1.218 B33=  -0.411
REMARK    B12=   0.000 B13=   0.000 B23=   0.000
REMARK B-factor correction applied to coordinate array B:   -0.233
REMARK bulk solvent: (Mask)density level= 0.31769 e/A^3, B-factor=51.8227 A^2
REMARK reflections with |Fobs|/sigma_F < 0.0 rejected
REMARK reflections with |Fobs| > 10000 * rms(Fobs) rejected
REMARK theoretical total number of refl. in resol. range:     36279(100.0 % )
REMARK number of unobserved reflections (no entry or |F|=0):   9992 (27.5 % )
REMARK number of reflections rejected:                            0 ( 0.0 % )
REMARK total number of reflections used:                      26287 (72.5 % )
REMARK number of reflections in working set:                  25018 (69.0 % )
REMARK number of reflections in test set:                      1269 ( 3.5 % )
REMARK FILENAME="bindividual.pdb"
REMARK DATE:Feb-12-2001  13:11:17       created by user: mar345
REMARK Written by CNX VERSION:2000.1
CRYST1   52.603   88.421   67.832  90.00  90.01  90.00 P 1 21 1
SCALE1      0.019010  0.000000  0.000003        0.00000
SCALE2      0.000000  0.011310  0.000000        0.00000
SCALE3      0.000000  0.000000  0.014742        0.00000
ATOM      1  CB  GLN A 126      32.162 112.290  73.232  1.00 49.44      A    C
ATOM      2  CG  GLN A 126      32.015 113.484  72.284  1.00 51.02      A    C
ATOM      3  CD  GLN A 126      32.563 113.219  70.887  1.00 51.57      A    C
ATOM      4  OE1 GLN A 126      31.961 112.499  70.089  1.00 51.89      A    O
ATOM      5  NE2 GLN A 126      33.717 113.803  70.589  1.00 52.45      A    N
ATOM      6  C   GLN A 126      31.499 110.010  73.975  1.00 46.32      A    C
ATOM      7  O   GLN A 126      31.745 110.223  75.161  1.00 48.00      A    O
ATOM      8  N   GLN A 126      29.765 111.655  73.328  1.00 47.98      A    N
ATOM      9  CA  GLN A 126      31.143 111.162  73.040  1.00 47.45      A    C
ATOM     10  N   TRP A 127      31.523 108.792  73.443  1.00 43.51      A    N
ATOM     11  CA  TRP A 127      31.864 107.618  74.238  1.00 40.38      A    C
ATOM     12  CB  TRP A 127      30.998 106.418  73.836  1.00 40.28      A    C
ATOM     13  CG  TRP A 127      29.528 106.692  73.786  1.00 37.53      A    C
ATOM     14  CD2 TRP A 127      28.575 106.442  74.826  1.00 36.46      A    C
ATOM     15  CE2 TRP A 127      27.309 106.835  74.335  1.00 36.39      A    C
ATOM     16  CE3 TRP A 127      28.669 105.924  76.123  1.00 34.75      A    C
ATOM     17  CD1 TRP A 127      28.827 107.215  72.740  1.00 37.84      A    C
```

	ATOM	18	NE1	TRP	A 127	27.490	107.302	73.060	1.00	36.81	A N
	ATOM	19	CZ2	TRP	A 127	26.142	106.725	75.097	1.00	36.10	A C
	ATOM	20	CZ3	TRP	A 127	27.507	105.814	76.884	1.00	37.35	A C
	ATOM	21	CH2	TRP	A 127	26.260	106.214	76.366	1.00	37.47	A C
5	ATOM	22	C	TRP	A 127	33.329	107.249	74.024	1.00	38.84	A C
	ATOM	23	O	TRP	A 127	33.984	107.765	73.117	1.00	37.85	A O
	ATOM	24	N	ALA	A 128	33.835	106.349	74.858	1.00	36.22	A N
	ATOM	25	CA	ALA	A 128	35.212	105.891	74.741	1.00	35.97	A C
	ATOM	26	CB	ALA	A 128	36.136	106.763	75.582	1.00	35.91	A C
10	ATOM	27	C	ALA	A 128	35.289	104.441	75.200	1.00	35.31	A C
	ATOM	28	O	ALA	A 128	34.514	104.015	76.056	1.00	34.64	A O
	ATOM	29	N	LEU	A 129	36.221	103.688	74.626	1.00	33.98	A N
	ATOM	30	CA	LEU	A 129	36.385	102.283	74.976	1.00	34.14	A C
	ATOM	31	CB	LEU	A 129	37.556	101.681	74.191	1.00	33.48	A C
15	ATOM	32	CG	LEU	A 129	37.816	100.175	74.339	1.00	35.39	A C
	ATOM	33	CD1	LEU	A 129	36.514	99.396	74.175	1.00	34.09	A C
	ATOM	34	CD2	LEU	A 129	38.841	99.729	73.300	1.00	33.75	A C
	ATOM	35	C	LEU	A 129	36.596	102.092	76.476	1.00	33.77	A C
	ATOM	36	O	LEU	A 129	36.028	101.182	77.083	1.00	33.18	A O
20	ATOM	37	N	ALA	A 130	37.389	102.974	77.072	1.00	34.08	A N
	ATOM	38	CA	ALA	A 130	37.691	102.918	78.500	1.00	33.53	A C
	ATOM	39	CB	ALA	A 130	38.757	103.954	78.836	1.00	33.52	A C
	ATOM	40	C	ALA	A 130	36.483	103.112	79.415	1.00	33.70	A C
	ATOM	41	O	ALA	A 130	36.615	103.026	80.633	1.00	35.42	A O
25	ATOM	42	N	ASP	A 131	35.315	103.380	78.841	1.00	33.03	A N
	ATOM	43	CA	ASP	A 131	34.092	103.588	79.632	1.00	31.53	A C
	ATOM	44	CB	ASP	A 131	33.094	104.444	78.849	1.00	35.30	A C
	ATOM	45	CG	ASP	A 131	33.415	105.919	78.898	1.00	37.25	A C
	ATOM	46	OD1	ASP	A 131	32.854	106.665	78.066	1.00	40.43	A O
30	ATOM	47	OD2	ASP	A 131	34.209	106.335	79.770	1.00	39.65	A O
	ATOM	48	C	ASP	A 131	33.404	102.274	79.970	1.00	29.88	A C
	ATOM	49	O	ASP	A 131	32.510	102.223	80.816	1.00	27.49	A O
	ATOM	50	N	PHE	A 132	33.836	101.211	79.305	1.00	28.87	A N
	ATOM	51	CA	PHE	A 132	33.232	99.906	79.487	1.00	27.75	A C
35	ATOM	52	CB	PHE	A 132	32.617	99.450	78.168	1.00	25.08	A C
	ATOM	53	CG	PHE	A 132	31.820	100.504	77.478	1.00	24.75	A C
	ATOM	54	CD1	PHE	A 132	30.535	100.808	77.899	1.00	22.62	A C
	ATOM	55	CD2	PHE	A 132	32.356	101.195	76.403	1.00	22.91	A C
	ATOM	56	CE1	PHE	A 132	29.794	101.788	77.249	1.00	26.12	A C
40	ATOM	57	CE2	PHE	A 132	31.626	102.174	75.749	1.00	25.55	A C
	ATOM	58	CZ	PHE	A 132	30.340	102.471	76.173	1.00	23.27	A C
	ATOM	59	C	PHE	A 132	34.164	98.801	79.947	1.00	27.73	A C
	ATOM	60	O	PHE	A 132	35.375	98.852	79.736	1.00	27.55	A O
	ATOM	61	N	GLU	A 133	33.560	97.798	80.575	1.00	27.29	A N
45	ATOM	62	CA	GLU	A 133	34.254	96.596	81.004	1.00	26.91	A C
	ATOM	63	CB	GLU	A 133	33.863	96.187	82.415	1.00	29.96	A C
	ATOM	64	CG	GLU	A 133	34.290	97.120	83.506	1.00	35.88	A C
	ATOM	65	CD	GLU	A 133	33.945	96.546	84.858	1.00	39.31	A C
	ATOM	66	OE1	GLU	A 133	34.491	95.469	85.189	1.00	40.33	A O
50	ATOM	67	OE2	GLU	A 133	33.120	97.153	85.576	1.00	40.57	A O
	ATOM	68	C	GLU	A 133	33.665	95.582	80.034	1.00	24.82	A C
	ATOM	69	O	GLU	A 133	32.444	95.536	79.854	1.00	21.66	A O
	ATOM	70	N	ILE	A 134	34.523	94.787	79.410	1.00	22.94	A N
	ATOM	71	CA	ILE	A 134	34.091	93.784	78.443	1.00	22.52	A C
55	ATOM	72	CB	ILE	A 134	35.115	93.688	77.286	1.00	23.20	A C
	ATOM	73	CG2	ILE	A 134	34.652	92.704	76.240	1.00	23.57	A C
	ATOM	74	CG1	ILE	A 134	35.317	95.073	76.668	1.00	26.34	A C
	ATOM	75	CD1	ILE	A 134	34.059	95.709	76.121	1.00	27.45	A C
	ATOM	76	C	ILE	A 134	33.935	92.413	79.093	1.00	23.10	A C
60	ATOM	77	O	ILE	A 134	34.737	92.024	79.941	1.00	24.84	A O
	ATOM	78	N	GLY	A 135	32.904	91.679	78.681	1.00	24.78	A N
	ATOM	79	CA	GLY	A 135	32.648	90.355	79.231	1.00	22.02	A C
	ATOM	80	C	GLY	A 135	32.677	89.246	78.193	1.00	20.46	A C
	ATOM	81	O	GLY	A 135	33.404	89.330	77.212	1.00	18.06	A O
65	ATOM	82	N	ARG	A 136	31.867	88.212	78.391	1.00	23.35	A N
	ATOM	83	CA	ARG	A 136	31.852	87.077	77.464	1.00	25.21	A C
	ATOM	84	CB	ARG	A 136	31.078	85.902	78.064	1.00	26.99	A C
	ATOM	85	CG	ARG	A 136	29.601	86.174	78.284	1.00	28.67	A C
	ATOM	86	CD	ARG	A 136	28.870	84.914	78.725	1.00	29.20	A C
70	ATOM	87	NE	ARG	A 136	27.497	85.201	79.121	1.00	31.23	A N
	ATOM	88	CZ	ARG	A 136	26.417	84.687	78.532	1.00	34.58	A C
	ATOM	89	NH1	ARG	A 136	26.546	83.847	77.512	1.00	33.49	A N

ATOM	90	NH2	ARG	A	136	25.204	85.028	78.958	1.00	34.12	A N
ATOM	91	C	ARG	A	136	31.285	87.369	76.084	1.00	26.22	A C
ATOM	92	O	ARG	A	136	30.450	88.260	75.916	1.00	24.47	A O
ATOM	93	N	PRO	A	137	31.749	86.620	75.070	1.00	26.55	A N
ATOM	94	CD	PRO	A	137	32.907	85.714	75.122	1.00	27.27	A C
ATOM	95	CA	PRO	A	137	31.285	86.786	73.690	1.00	26.49	A C
ATOM	96	CB	PRO	A	137	32.236	85.898	72.887	1.00	25.92	A C
ATOM	97	CG	PRO	A	137	33.477	85.858	73.729	1.00	25.14	A C
ATOM	98	C	PRO	A	137	29.856	86.276	73.609	1.00	27.01	A C
ATOM	99	O	PRO	A	137	29.538	85.226	74.169	1.00	26.92	A O
ATOM	100	N	LEU	A	138	28.995	87.018	72.924	1.00	27.88	A N
ATOM	101	CA	LEU	A	138	27.602	86.615	72.779	1.00	29.09	A C
ATOM	102	CB	LEU	A	138	26.691	87.843	72.865	1.00	27.78	A C
ATOM	103	CG	LEU	A	138	26.450	88.473	74.240	1.00	26.22	A C
ATOM	104	CD1	LEU	A	138	27.758	88.636	74.965	1.00	29.17	A C
ATOM	105	CD2	LEU	A	138	25.771	89.816	74.075	1.00	20.07	A C
ATOM	106	C	LEU	A	138	27.403	85.907	71.438	1.00	30.81	A C
ATOM	107	O	LEU	A	138	26.619	84.964	71.329	1.00	32.24	A O
ATOM	108	N	GLY	A	139	28.124	86.367	70.424	1.00	32.34	A N
ATOM	109	CA	GLY	A	139	28.014	85.773	69.109	1.00	35.00	A C
ATOM	110	C	GLY	A	139	29.136	86.215	68.190	1.00	38.07	A C
ATOM	111	O	GLY	A	139	29.859	87.166	68.488	1.00	38.60	A O
ATOM	112	N	LYS	A	140	29.281	85.519	67.066	1.00	41.32	A N
ATOM	113	CA	LYS	A	140	30.320	85.831	66.092	1.00	43.10	A C
ATOM	114	CB	LYS	A	140	31.244	84.633	65.917	1.00	44.15	A C
ATOM	115	C	LYS	A	140	29.703	86.216	64.751	1.00	44.25	A C
ATOM	116	O	LYS	A	140	28.615	85.755	64.403	1.00	43.38	A O
ATOM	117	N	GLY	A	141	30.406	87.066	64.007	1.00	45.98	A N
ATOM	118	CA	GLY	A	141	29.939	87.527	62.705	1.00	47.85	A C
ATOM	119	CB	GLY	A	141	29.270	88.895	62.842	1.00	49.28	A C
ATOM	120	C	GLY	A	141	31.109	87.613	61.731	1.00	48.68	A C
ATOM	121	O	GLY	A	141	32.235	87.245	62.073	1.00	48.92	A O
ATOM	122	N	ALA	A	142	30.842	88.111	60.525	1.00	48.78	A N
ATOM	123	CA	ALA	A	142	31.877	88.226	59.502	1.00	47.65	A C
ATOM	124	CB	ALA	A	142	31.247	88.156	58.115	1.00	48.08	A C
ATOM	125	C	ALA	A	142	32.730	89.488	59.620	1.00	46.86	A C
ATOM	126	O	ALA	A	142	33.828	89.550	59.063	1.00	46.94	A O
ATOM	127	N	PHE	A	143	32.242	90.492	60.343	1.00	45.34	A N
ATOM	128	CA	PHE	A	143	33.004	91.731	60.477	1.00	43.93	A C
ATOM	129	CB	PHE	A	143	32.193	92.907	59.920	1.00	43.56	A C
ATOM	130	CG	PHE	A	143	31.628	92.653	58.550	1.00	43.95	A C
ATOM	131	CD1	PHE	A	143	30.352	92.118	58.397	1.00	44.56	A C
ATOM	132	CD2	PHE	A	143	32.385	92.915	57.413	1.00	44.21	A C
ATOM	133	CE1	PHE	A	143	29.836	91.845	57.129	1.00	44.68	A C
ATOM	134	CE2	PHE	A	143	31.881	92.645	56.141	1.00	44.72	A C
ATOM	135	CZ	PHE	A	143	30.604	92.109	55.999	1.00	44.72	A C
ATOM	136	C	PHE	A	143	33.456	92.045	61.901	1.00	42.13	A C
ATOM	137	O	PHE	A	143	34.137	93.043	62.132	1.00	41.48	A O
ATOM	138	N	GLY	A	144	33.085	91.183	62.846	1.00	40.73	A N
ATOM	139	CA	GLY	A	144	33.452	91.396	64.235	1.00	37.57	A C
ATOM	140	C	GLY	A	144	32.537	90.631	65.171	1.00	36.23	A C
ATOM	141	O	GLY	A	144	31.625	89.938	64.721	1.00	35.58	A O
ATOM	142	N	ASN	A	145	32.763	90.763	66.474	1.00	34.55	A N
ATOM	143	CA	ASN	A	145	31.947	90.052	67.453	1.00	32.65	A C
ATOM	144	CB	ASN	A	145	32.842	89.187	68.341	1.00	34.14	A C
ATOM	145	CG	ASN	A	145	33.913	88.458	67.549	1.00	36.27	A C
ATOM	146	OD1	ASN	A	145	35.068	88.893	67.489	1.00	36.74	A O
ATOM	147	ND2	ASN	A	145	33.531	87.352	66.924	1.00	35.73	A N
ATOM	148	C	ASN	A	145	31.096	90.959	68.331	1.00	30.37	A C
ATOM	149	O	ASN	A	145	31.232	92.183	68.308	1.00	31.36	A O
ATOM	150	N	VAL	A	146	30.214	90.337	69.107	1.00	27.53	A N
ATOM	151	CA	VAL	A	146	29.326	91.051	70.013	1.00	24.74	A C
ATOM	152	CB	VAL	A	146	27.836	90.769	69.684	1.00	26.28	A C
ATOM	153	CG1	VAL	A	146	26.932	91.644	70.548	1.00	24.90	A C
ATOM	154	CG2	VAL	A	146	27.573	91.006	68.211	1.00	28.46	A C
ATOM	155	C	VAL	A	146	29.605	90.546	71.424	1.00	22.82	A C
ATOM	156	O	VAL	A	146	29.599	89.341	71.660	1.00	24.33	A O
ATOM	157	N	TYR	A	147	29.836	91.461	72.357	1.00	20.11	A N
ATOM	158	CA	TYR	A	147	30.125	91.081	73.738	1.00	18.69	A C
ATOM	159	CB	TYR	A	147	31.530	91.523	74.145	1.00	16.30	A C
ATOM	160	CG	TYR	A	147	32.646	91.083	73.231	1.00	20.13	A C
ATOM	161	CD1	TYR	A	147	32.849	91.701	71.997	1.00	19.62	A C

ATOM	162	CE1	TYR	A	147	33.898	91.318	71.162	1.00	22.76	A C
ATOM	163	CD2	TYR	A	147	33.519	90.059	73.610	1.00	19.37	A C
ATOM	164	CE2	TYR	A	147	34.574	89.661	72.777	1.00	20.22	A C
ATOM	165	CZ	TYR	A	147	34.755	90.298	71.559	1.00	23.88	A C
ATOM	166	OH	TYR	A	147	35.788	89.925	70.727	1.00	27.07	A O
ATOM	167	C	TYR	A	147	29.177	91.690	74.757	1.00	17.31	A C
ATOM	168	O	TYR	A	147	28.568	92.731	74.521	1.00	16.25	A O
ATOM	169	N	LEU	A	148	29.071	91.026	75.903	1.00	17.91	A N
ATOM	170	CA	LEU	A	148	28.283	91.544	76.996	1.00	16.28	A C
ATOM	171	CB	LEU	A	148	28.040	90.472	78.054	1.00	19.47	A C
ATOM	172	CG	LEU	A	148	27.148	90.939	79.205	1.00	19.54	A C
ATOM	173	CD1	LEU	A	148	25.844	90.198	79.117	1.00	23.07	A C
ATOM	174	CD2	LEU	A	148	27.809	90.695	80.561	1.00	21.88	A C
ATOM	175	C	LEU	A	148	29.230	92.599	77.555	1.00	16.81	A C
ATOM	176	O	LEU	A	148	30.449	92.387	77.604	1.00	17.66	A O
ATOM	177	N	ALA	A	149	28.693	93.740	77.962	1.00	17.06	A N
ATOM	178	CA	ALA	A	149	29.529	94.794	78.504	1.00	15.77	A C
ATOM	179	CB	ALA	A	149	29.953	95.744	77.400	1.00	16.74	A C
ATOM	180	C	ALA	A	149	28.778	95.540	79.591	1.00	19.32	A C
ATOM	181	O	ALA	A	149	27.585	95.302	79.815	1.00	17.25	A O
ATOM	182	N	ARG	A	150	29.483	96.442	80.262	1.00	18.18	A N
ATOM	183	CA	ARG	A	150	28.903	97.215	81.338	1.00	20.87	A C
ATOM	184	CB	ARG	A	150	29.073	96.435	82.651	1.00	24.33	A C
ATOM	185	CG	ARG	A	150	28.543	97.119	83.890	1.00	30.19	A C
ATOM	186	CD	ARG	A	150	28.249	96.096	84.995	1.00	32.40	A C
ATOM	187	NE	ARG	A	150	29.370	95.162	85.167	1.00	33.70	A N
ATOM	188	CZ	ARG	A	150	29.308	94.053	85.897	1.00	35.11	A C
ATOM	189	NH1	ARG	A	150	28.186	93.735	86.533	1.00	36.02	A N
ATOM	190	NH2	ARG	A	150	30.365	93.252	85.983	1.00	32.01	A N
ATOM	191	C	ARG	A	150	29.593	98.574	81.422	1.00	22.84	A C
ATOM	192	O	ARG	A	150	30.808	98.675	81.180	1.00	18.77	A O
ATOM	193	N	GLU	A	151	28.819	99.618	81.727	1.00	23.89	A N
ATOM	194	CA	GLU	A	151	29.383	100.958	81.874	1.00	26.53	A C
ATOM	195	CB	GLU	A	151	28.286	102.033	81.883	1.00	26.52	A C
ATOM	196	CG	GLU	A	151	27.420	102.099	80.629	1.00	28.40	A C
ATOM	197	CD	GLU	A	151	26.365	103.198	80.704	1.00	29.97	A C
ATOM	198	OE1	GLU	A	151	25.724	103.337	81.765	1.00	29.43	A O
ATOM	199	OE2	GLU	A	151	26.164	103.917	79.704	1.00	31.53	A O
ATOM	200	C	GLU	A	151	30.049	100.897	83.242	1.00	27.68	A C
ATOM	201	O	GLU	A	151	29.390	100.577	84.230	1.00	28.40	A O
ATOM	202	N	LYS	A	152	31.346	101.195	83.288	1.00	30.73	A N
ATOM	203	CA	LYS	A	152	32.135	101.140	84.523	1.00	33.53	A C
ATOM	204	CB	LYS	A	152	33.545	101.691	84.288	1.00	34.64	A C
ATOM	205	CG	LYS	A	152	34.448	100.758	83.531	1.00	37.25	A C
ATOM	206	CD	LYS	A	152	35.836	101.367	83.353	1.00	39.94	A C
ATOM	207	CE	LYS	A	152	36.759	100.408	82.629	1.00	40.54	A C
ATOM	208	NZ	LYS	A	152	38.093	101.012	82.399	1.00	41.98	A N
ATOM	209	C	LYS	A	152	31.548	101.842	85.727	1.00	33.54	A C
ATOM	210	O	LYS	A	152	31.401	101.239	86.790	1.00	35.42	A O
ATOM	211	N	GLN	A	153	31.222	103.117	85.564	1.00	33.48	A N
ATOM	212	CA	GLN	A	153	30.669	103.904	86.655	1.00	34.22	A C
ATOM	213	CB	GLN	A	153	30.568	105.370	86.231	1.00	36.43	A C
ATOM	214	CG	GLN	A	153	31.890	105.975	85.797	1.00	39.77	A C
ATOM	215	CD	GLN	A	153	32.954	105.939	86.889	1.00	42.68	A C
ATOM	216	OE1	GLN	A	153	34.107	106.304	86.657	1.00	46.22	A O
ATOM	217	NE2	GLN	A	153	32.572	105.503	88.082	1.00	43.83	A N
ATOM	218	C	GLN	A	153	29.316	103.424	87.182	1.00	33.78	A C
ATOM	219	O	GLN	A	153	29.226	102.938	88.314	1.00	34.62	A O
ATOM	220	N	SER	A	154	28.268	103.555	86.371	1.00	32.03	A N
ATOM	221	CA	SER	A	154	26.929	103.156	86.794	1.00	29.99	A C
ATOM	222	CB	SER	A	154	25.868	103.831	85.914	1.00	29.69	A C
ATOM	223	OG	SER	A	154	26.050	103.510	84.551	1.00	29.28	A O
ATOM	224	C	SER	A	154	26.661	101.657	86.845	1.00	29.81	A C
ATOM	225	O	SER	A	154	25.646	101.236	87.398	1.00	29.38	A O
ATOM	226	N	LYS	A	155	27.550	100.855	86.261	1.00	29.05	A N
ATOM	227	CA	LYS	A	155	27.389	99.401	86.276	1.00	30.67	A C
ATOM	228	CB	LYS	A	155	27.185	98.936	87.725	1.00	32.82	A C
ATOM	229	CG	LYS	A	155	27.059	97.435	87.912	1.00	39.02	A C
ATOM	230	CD	LYS	A	155	26.671	97.066	89.342	1.00	43.54	A C
ATOM	231	CE	LYS	A	155	25.205	97.386	89.669	1.00	47.18	A C
ATOM	232	NZ	LYS	A	155	24.902	98.848	89.800	1.00	49.30	A N
ATOM	233	C	LYS	A	155	26.223	98.913	85.398	1.00	28.46	A C

ATOM	234	O	LYS	A	155	25.706	97.812	85.590	1.00	27.89	A	O
ATOM	235	N	PHE	A	156	25.831	99.727	84.424	1.00	26.49	A	N
ATOM	236	CA	PHE	A	156	24.716	99.403	83.536	1.00	23.82	A	C
ATOM	237	CB	PHE	A	156	24.185	100.698	82.905	1.00	24.31	A	C
ATOM	238	CG	PHE	A	156	23.043	100.492	81.955	1.00	24.97	A	C
ATOM	239	CD1	PHE	A	156	21.771	100.187	82.428	1.00	24.81	A	C
ATOM	240	CD2	PHE	A	156	23.244	100.592	80.580	1.00	24.41	A	C
ATOM	241	CE1	PHE	A	156	20.705	99.982	81.537	1.00	27.89	A	C
ATOM	242	CE2	PHE	A	156	22.195	100.390	79.685	1.00	24.55	A	C
ATOM	243	CZ	PHE	A	156	20.920	100.084	80.163	1.00	25.32	A	C
ATOM	244	C	PHE	A	156	25.082	98.381	82.445	1.00	21.90	A	C
ATOM	245	O	PHE	A	156	26.019	98.582	81.676	1.00	21.26	A	O
ATOM	246	N	ILE	A	157	24.321	97.294	82.388	1.00	19.42	A	N
ATOM	247	CA	ILE	A	157	24.535	96.219	81.418	1.00	19.66	A	C
ATOM	248	CB	ILE	A	157	23.863	94.906	81.878	1.00	20.30	A	C
ATOM	249	CG2	ILE	A	157	23.931	93.876	80.759	1.00	18.66	A	C
ATOM	250	CG1	ILE	A	157	24.541	94.373	83.143	1.00	20.54	A	C
ATOM	251	CD1	ILE	A	157	25.994	93.979	82.929	1.00	23.70	A	C
ATOM	252	C	ILE	A	157	23.996	96.515	80.018	1.00	20.08	A	C
ATOM	253	O	ILE	A	157	22.851	96.955	79.859	1.00	18.61	A	O
ATOM	254	N	LEU	A	158	24.819	96.239	79.011	1.00	18.01	A	N
ATOM	255	CA	LEU	A	158	24.445	96.436	77.616	1.00	19.34	A	C
ATOM	256	CB	LEU	A	158	24.651	97.900	77.220	1.00	20.73	A	C
ATOM	257	CG	LEU	A	158	25.882	98.644	77.734	1.00	22.83	A	C
ATOM	258	CD1	LEU	A	158	27.125	98.226	76.965	1.00	23.65	A	C
ATOM	259	CD2	LEU	A	158	25.633	100.139	77.576	1.00	24.53	A	C
ATOM	260	C	LEU	A	158	25.231	95.498	76.688	1.00	19.24	A	C
ATOM	261	O	LEU	A	158	25.944	94.623	77.153	1.00	20.32	A	O
ATOM	262	N	ALA	A	159	25.077	95.654	75.379	1.00	19.56	A	N
ATOM	263	CA	ALA	A	159	25.790	94.803	74.431	1.00	19.83	A	C
ATOM	264	CB	ALA	A	159	24.809	94.009	73.579	1.00	19.54	A	C
ATOM	265	C	ALA	A	159	26.673	95.672	73.553	1.00	20.25	A	C
ATOM	266	O	ALA	A	159	26.274	96.766	73.143	1.00	19.23	A	O
ATOM	267	N	LEU	A	160	27.878	95.190	73.274	1.00	20.17	A	N
ATOM	268	CA	LEU	A	160	28.820	95.944	72.459	1.00	22.21	A	C
ATOM	269	CB	LEU	A	160	30.019	96.360	73.326	1.00	23.33	A	C
ATOM	270	CG	LEU	A	160	31.194	97.129	72.715	1.00	27.33	A	C
ATOM	271	CD1	LEU	A	160	30.789	98.572	72.410	1.00	27.43	A	C
ATOM	272	CD2	LEU	A	160	32.359	97.112	73.699	1.00	26.63	A	C
ATOM	273	C	LEU	A	160	29.292	95.146	71.249	1.00	22.33	A	C
ATOM	274	O	LEU	A	160	29.772	94.021	71.379	1.00	21.48	A	O
ATOM	275	N	LYS	A	161	29.170	95.738	70.067	1.00	23.83	A	N
ATOM	276	CA	LYS	A	161	29.612	95.082	68.840	1.00	24.70	A	C
ATOM	277	CB	LYS	A	161	28.502	95.107	67.792	1.00	24.56	A	C
ATOM	278	CG	LYS	A	161	28.735	94.154	66.635	1.00	26.78	A	C
ATOM	279	CD	LYS	A	161	27.431	93.891	65.887	1.00	25.97	A	C
ATOM	280	CE	LYS	A	161	27.612	92.863	64.792	1.00	23.17	A	C
ATOM	281	NZ	LYS	A	161	26.293	92.377	64.315	1.00	22.83	A	N
ATOM	282	C	LYS	A	161	30.850	95.798	68.314	1.00	25.61	A	C
ATOM	283	O	LYS	A	161	30.850	97.014	68.146	1.00	25.29	A	O
ATOM	284	N	VAL	A	162	31.907	95.031	68.072	1.00	27.06	A	N
ATOM	285	CA	VAL	A	162	33.172	95.568	67.585	1.00	28.41	A	C
ATOM	286	CB	VAL	A	162	34.346	95.050	68.456	1.00	31.04	A	C
ATOM	287	CG1	VAL	A	162	35.678	95.617	67.957	1.00	31.63	A	C
ATOM	288	CG2	VAL	A	162	34.113	95.427	69.914	1.00	30.41	A	C
ATOM	289	C	VAL	A	162	33.387	95.132	66.139	1.00	28.72	A	C
ATOM	290	O	VAL	A	162	33.387	93.942	65.844	1.00	28.91	A	O
ATOM	291	N	LEU	A	163	33.561	96.096	65.241	1.00	30.09	A	N
ATOM	292	CA	LEU	A	163	33.760	95.801	63.823	1.00	31.38	A	C
ATOM	293	CB	LEU	A	163	32.670	96.479	62.987	1.00	30.68	A	C
ATOM	294	CG	LEU	A	163	31.207	96.151	63.295	1.00	31.65	A	C
ATOM	295	CD1	LEU	A	163	30.343	97.379	63.035	1.00	33.15	A	C
ATOM	296	CD2	LEU	A	163	30.747	94.985	62.452	1.00	31.46	A	C
ATOM	297	C	LEU	A	163	35.116	96.333	63.393	1.00	32.77	A	C
ATOM	298	O	LEU	A	163	35.541	97.386	63.865	1.00	33.03	A	O
ATOM	299	N	PHE	A	164	35.793	95.610	62.503	1.00	34.61	A	N
ATOM	300	CA	PHE	A	164	37.107	96.043	62.018	1.00	36.93	A	C
ATOM	301	CB	PHE	A	164	38.068	94.849	61.878	1.00	38.68	A	C
ATOM	302	CG	PHE	A	164	38.406	94.181	63.180	1.00	40.41	A	C
ATOM	303	CD1	PHE	A	164	37.659	93.101	63.639	1.00	41.41	A	C
ATOM	304	CD2	PHE	A	164	39.464	94.645	63.960	1.00	41.14	A	C
ATOM	305	CE1	PHE	A	164	37.959	92.489	64.857	1.00	41.57	A	C

ATOM	306	CE2	PHE	A	164	39.774	94.041	65.182	1.00	42.28	A C
ATOM	307	CZ	PHE	A	164	39.020	92.960	65.630	1.00	41.55	A C
ATOM	308	C	PHE	A	164	37.000	96.759	60.674	1.00	36.27	A C
ATOM	309	O	PHE	A	164	36.489	96.203	59.701	1.00	34.52	A O
ATOM	310	N	LYS	A	165	37.495	97.993	60.632	1.00	37.51	A N
ATOM	311	CA	LYS	A	165	37.461	98.809	59.422	1.00	39.00	A C
ATOM	312	CB	LYS	A	165	38.248	100.103	59.635	1.00	39.41	A C
ATOM	313	CG	LYS	A	165	37.700	100.988	60.738	1.00	41.43	A C
ATOM	314	CD	LYS	A	165	38.473	102.292	60.820	1.00	43.19	A C
ATOM	315	CE	LYS	A	165	37.957	103.175	61.941	1.00	43.06	A C
ATOM	316	NZ	LYS	A	165	38.712	104.452	62.007	1.00	45.01	A N
ATOM	317	C	LYS	A	165	38.016	98.092	58.200	1.00	39.84	A C
ATOM	318	O	LYS	A	165	37.332	97.966	57.183	1.00	40.35	A O
ATOM	319	N	ALA	A	166	39.259	97.629	58.309	1.00	40.50	A N
ATOM	320	CA	ALA	A	166	39.930	96.930	57.218	1.00	41.24	A C
ATOM	321	CB	ALA	A	166	41.230	96.314	57.717	1.00	40.66	A C
ATOM	322	C	ALA	A	166	39.039	95.850	56.622	1.00	42.45	A C
ATOM	323	O	ALA	A	166	39.143	95.524	55.439	1.00	42.34	A O
ATOM	324	N	GLN	A	167	38.160	95.298	57.448	1.00	42.58	A N
ATOM	325	CA	GLN	A	167	37.256	94.255	56.995	1.00	44.47	A C
ATOM	326	CB	GLN	A	167	36.814	93.405	58.189	1.00	47.08	A C
ATOM	327	CG	GLN	A	167	36.076	92.133	57.818	1.00	49.82	A C
ATOM	328	CD	GLN	A	167	36.382	90.991	58.772	1.00	51.86	A C
ATOM	329	OE1	GLN	A	167	36.182	91.105	59.985	1.00	52.31	A O
ATOM	330	NE2	GLN	A	167	36.873	89.880	58.226	1.00	52.20	A N
ATOM	331	C	GLN	A	167	36.044	94.856	56.288	1.00	44.78	A C
ATOM	332	O	GLN	A	167	35.580	94.329	55.277	1.00	44.92	A O
ATOM	333	N	LEU	A	168	35.539	95.965	56.818	1.00	45.62	A N
ATOM	334	CA	LEU	A	168	34.379	96.635	56.232	1.00	47.56	A C
ATOM	335	CB	LEU	A	168	33.899	97.775	57.146	1.00	46.01	A C
ATOM	336	CG	LEU	A	168	33.222	97.423	58.476	1.00	43.92	A C
ATOM	337	CD1	LEU	A	168	33.079	98.664	59.335	1.00	42.28	A C
ATOM	338	CD2	LEU	A	168	31.866	96.802	58.209	1.00	44.54	A C
ATOM	339	C	LEU	A	168	34.702	97.200	54.851	1.00	49.49	A C
ATOM	340	O	LEU	A	168	33.974	96.973	53.884	1.00	49.80	A O
ATOM	341	N	GLU	A	169	35.806	97.930	54.756	1.00	51.68	A N
ATOM	342	CA	GLU	A	169	36.185	98.536	53.490	1.00	53.42	A C
ATOM	343	CB	GLU	A	169	37.063	99.751	53.749	1.00	53.84	A C
ATOM	344	CG	GLU	A	169	38.381	99.423	54.394	1.00	54.96	A C
ATOM	345	CD	GLU	A	169	39.178	100.665	54.697	1.00	55.82	A C
ATOM	346	OE1	GLU	A	169	38.781	101.410	55.619	1.00	55.83	A O
ATOM	347	OE2	GLU	A	169	40.193	100.901	54.006	1.00	57.62	A O
ATOM	348	C	GLU	A	169	36.886	97.589	52.523	1.00	53.75	A C
ATOM	349	O	GLU	A	169	37.892	97.947	51.922	1.00	54.54	A O
ATOM	350	N	LYS	A	170	36.352	96.382	52.375	1.00	54.68	A N
ATOM	351	CA	LYS	A	170	36.923	95.398	51.464	1.00	55.27	A C
ATOM	352	CB	LYS	A	170	38.040	94.603	52.151	1.00	56.80	A C
ATOM	353	CG	LYS	A	170	37.588	93.641	53.249	1.00	59.09	A C
ATOM	354	CD	LYS	A	170	37.396	92.216	52.725	1.00	59.63	A C
ATOM	355	CE	LYS	A	170	37.133	91.239	53.873	1.00	60.14	A C
ATOM	356	NZ	LYS	A	170	37.117	89.809	53.437	1.00	59.19	A N
ATOM	357	C	LYS	A	170	35.815	94.469	50.997	1.00	55.75	A C
ATOM	358	O	LYS	A	170	35.765	94.086	49.830	1.00	56.27	A O
ATOM	359	N	ALA	A	171	34.921	94.116	51.915	1.00	55.93	A N
ATOM	360	CA	ALA	A	171	33.792	93.250	51.590	1.00	56.64	A C
ATOM	361	CB	ALA	A	171	33.064	92.823	52.866	1.00	56.68	A C
ATOM	362	C	ALA	A	171	32.876	94.088	50.719	1.00	56.98	A C
ATOM	363	O	ALA	A	171	31.899	93.599	50.139	1.00	55.93	A O
ATOM	364	N	GLY	A	172	33.207	95.369	50.642	1.00	56.93	A N
ATOM	365	CA	GLY	A	172	32.429	96.297	49.856	1.00	58.46	A C
ATOM	366	C	GLY	A	172	32.681	97.681	50.397	1.00	59.30	A C
ATOM	367	O	GLY	A	172	33.629	97.892	51.156	1.00	60.21	A O
ATOM	368	N	VAL	A	173	31.840	98.626	50.003	1.00	59.95	A N
ATOM	369	CA	VAL	A	173	31.970	99.998	50.459	1.00	60.15	A C
ATOM	370	CB	VAL	A	173	31.642	100.992	49.328	1.00	61.54	A C
ATOM	371	CG1	VAL	A	173	31.817	102.420	49.825	1.00	62.43	A C
ATOM	372	CG2	VAL	A	173	32.538	100.720	48.118	1.00	61.17	A C
ATOM	373	C	VAL	A	173	30.955	100.142	51.574	1.00	59.92	A C
ATOM	374	O	VAL	A	173	29.860	100.673	51.369	1.00	60.94	A O
ATOM	375	N	GLU	A	174	31.327	99.652	52.756	1.00	58.81	A N
ATOM	376	CA	GLU	A	174	30.452	99.681	53.921	1.00	55.71	A C
ATOM	377	CB	GLU	A	174	31.091	98.900	55.067	1.00	56.69	A C

ATOM	378	CG	GLU	A	174	31.360	97.440	54.731	1.00	57.20	A	C
ATOM	379	CD	GLU	A	174	30.135	96.717	54.197	1.00	57.78	A	C
ATOM	380	OE1	GLU	A	174	29.580	97.156	53.166	1.00	56.65	A	O
ATOM	381	OE2	GLU	A	174	29.733	95.705	54.808	1.00	57.97	A	O
ATOM	382	C	GLU	A	174	29.985	101.040	54.428	1.00	54.20	A	C
ATOM	383	O	GLU	A	174	29.998	101.302	55.634	1.00	53.74	A	O
ATOM	384	N	HIS	A	175	29.587	101.913	53.506	1.00	51.35	A	N
ATOM	385	CA	HIS	A	175	29.040	103.199	53.896	1.00	47.97	A	C
ATOM	386	CB	HIS	A	175	29.047	104.184	52.726	1.00	50.39	A	C
ATOM	387	CG	HIS	A	175	30.391	104.788	52.460	1.00	54.57	A	C
ATOM	388	CD2	HIS	A	175	30.998	105.144	51.303	1.00	55.04	A	C
ATOM	389	ND1	HIS	A	175	31.266	105.127	53.472	1.00	55.47	A	N
ATOM	390	CE1	HIS	A	175	32.354	105.664	52.949	1.00	55.64	A	C
ATOM	391	NE2	HIS	A	175	32.216	105.687	51.635	1.00	55.68	A	N
ATOM	392	C	HIS	A	175	27.615	102.794	54.253	1.00	44.77	A	C
ATOM	393	O	HIS	A	175	26.842	103.562	54.817	1.00	43.37	A	O
ATOM	394	N	GLN	A	176	27.299	101.550	53.902	1.00	41.61	A	N
ATOM	395	CA	GLN	A	176	26.010	100.942	54.178	1.00	39.54	A	C
ATOM	396	CB	GLN	A	176	25.982	99.524	53.604	1.00	40.25	A	C
ATOM	397	CG	GLN	A	176	24.822	98.672	54.086	1.00	42.14	A	C
ATOM	398	CD	GLN	A	176	23.480	99.184	53.606	1.00	44.16	A	C
ATOM	399	OE1	GLN	A	176	22.431	98.673	54.002	1.00	45.91	A	O
ATOM	400	NE2	GLN	A	176	23.505	100.193	52.745	1.00	43.65	A	N
ATOM	401	C	GLN	A	176	25.817	100.891	55.696	1.00	37.68	A	C
ATOM	402	O	GLN	A	176	24.727	101.142	56.205	1.00	36.70	A	O
ATOM	403	N	LEU	A	177	26.887	100.559	56.408	1.00	34.73	A	N
ATOM	404	CA	LEU	A	177	26.842	100.495	57.862	1.00	33.53	A	C
ATOM	405	CB	LEU	A	177	28.236	100.230	58.427	1.00	32.47	A	C
ATOM	406	CG	LEU	A	177	28.307	100.187	59.957	1.00	32.80	A	C
ATOM	407	CD1	LEU	A	177	27.773	98.844	60.439	1.00	33.65	A	C
ATOM	408	CD2	LEU	A	177	29.742	100.380	60.431	1.00	31.75	A	C
ATOM	409	C	LEU	A	177	26.357	101.842	58.380	1.00	33.15	A	C
ATOM	410	O	LEU	A	177	25.411	101.920	59.168	1.00	30.88	A	O
ATOM	411	N	ARG	A	178	27.021	102.898	57.916	1.00	31.91	A	N
ATOM	412	CA	ARG	A	178	26.709	104.261	58.317	1.00	31.40	A	C
ATOM	413	CB	ARG	A	178	27.661	105.238	57.618	1.00	33.75	A	C
ATOM	414	CG	ARG	A	178	27.658	106.625	58.226	1.00	36.73	A	C
ATOM	415	CD	ARG	A	178	28.681	107.531	57.562	1.00	43.53	A	C
ATOM	416	NE	ARG	A	178	28.822	108.809	58.262	1.00	46.96	A	N
ATOM	417	CZ	ARG	A	178	29.674	109.770	57.909	1.00	48.25	A	C
ATOM	418	NH1	ARG	A	178	30.466	109.604	56.857	1.00	48.99	A	N
ATOM	419	NH2	ARG	A	178	29.741	110.895	58.613	1.00	47.98	A	N
ATOM	420	C	ARG	A	178	25.254	104.669	58.065	1.00	29.09	A	C
ATOM	421	O	ARG	A	178	24.642	105.327	58.902	1.00	28.32	A	O
ATOM	422	N	ARG	A	179	24.694	104.289	56.924	1.00	28.97	A	N
ATOM	423	CA	ARG	A	179	23.301	104.633	56.624	1.00	27.69	A	C
ATOM	424	CB	ARG	A	179	22.907	104.220	55.194	1.00	29.53	A	C
ATOM	425	CG	ARG	A	179	23.091	105.294	54.131	1.00	33.34	A	C
ATOM	426	CD	ARG	A	179	22.514	104.813	52.800	1.00	34.69	A	C
ATOM	427	NE	ARG	A	179	21.091	104.473	52.896	1.00	38.29	A	N
ATOM	428	CZ	ARG	A	179	20.103	105.367	52.916	1.00	39.89	A	C
ATOM	429	NH1	ARG	A	179	20.377	106.665	52.842	1.00	41.81	A	N
ATOM	430	NH2	ARG	A	179	18.840	104.966	53.011	1.00	39.44	A	N
ATOM	431	C	ARG	A	179	22.377	103.900	57.589	1.00	25.80	A	C
ATOM	432	O	ARG	A	179	21.421	104.465	58.121	1.00	24.65	A	O
ATOM	433	N	GLU	A	180	22.689	102.628	57.795	1.00	24.97	A	N
ATOM	434	CA	GLU	A	180	21.924	101.746	58.655	1.00	24.64	A	C
ATOM	435	CB	GLU	A	180	22.475	100.329	58.512	1.00	25.95	A	C
ATOM	436	CG	GLU	A	180	21.507	99.239	58.900	1.00	30.77	A	C
ATOM	437	CD	GLU	A	180	20.238	99.256	58.073	1.00	32.75	A	C
ATOM	438	OE1	GLU	A	180	20.336	99.283	56.830	1.00	33.51	A	O
ATOM	439	OE2	GLU	A	180	19.138	99.233	58.669	1.00	36.77	A	O
ATOM	440	C	GLU	A	180	21.962	102.206	60.110	1.00	24.56	A	C
ATOM	441	O	GLU	A	180	20.965	102.116	60.831	1.00	23.69	A	O
ATOM	442	N	VAL	A	181	23.108	102.715	60.541	1.00	23.97	A	N
ATOM	443	CA	VAL	A	181	23.235	103.191	61.905	1.00	25.68	A	C
ATOM	444	CB	VAL	A	181	24.709	103.469	62.244	1.00	24.65	A	C
ATOM	445	CG1	VAL	A	181	24.806	104.314	63.499	1.00	21.02	A	C
ATOM	446	CG2	VAL	A	181	25.440	102.142	62.440	1.00	23.99	A	C
ATOM	447	C	VAL	A	181	22.403	104.459	62.100	1.00	27.42	A	C
ATOM	448	O	VAL	A	181	21.771	104.653	63.144	1.00	28.13	A	O
ATOM	449	N	GLU	A	182	22.406	105.307	61.079	1.00	28.83	A	N

ATOM	450	CA	GLU	A	182	21.667	106.563	61.092	1.00	31.06	A	C
ATOM	451	CB	GLU	A	182	21.938	107.314	59.779	1.00	34.99	A	C
ATOM	452	CG	GLU	A	182	21.403	108.753	59.671	1.00	41.26	A	C
ATOM	453	CD	GLU	A	182	21.846	109.429	58.359	1.00	45.14	A	C
ATOM	454	OE1	GLU	A	182	21.502	110.617	58.122	1.00	42.54	A	O
ATOM	455	OE2	GLU	A	182	22.548	108.757	57.561	1.00	46.92	A	O
ATOM	456	C	GLU	A	182	20.182	106.239	61.235	1.00	29.45	A	C
ATOM	457	O	GLU	A	182	19.488	106.798	62.080	1.00	26.72	A	O
ATOM	458	N	ILE	A	183	19.717	105.306	60.412	1.00	28.76	A	N
ATOM	459	CA	ILE	A	183	18.323	104.890	60.411	1.00	28.45	A	C
ATOM	460	CB	ILE	A	183	18.095	103.892	59.265	1.00	28.73	A	C
ATOM	461	CG2	ILE	A	183	16.618	103.413	59.318	1.00	28.72	A	C
ATOM	462	CG1	ILE	A	183	18.344	104.554	57.916	1.00	27.67	A	C
ATOM	463	CD1	ILE	A	183	18.250	103.605	56.728	1.00	26.58	A	C
ATOM	464	C	ILE	A	183	17.886	104.235	61.716	1.00	29.83	A	C
ATOM	465	O	ILE	A	183	16.870	104.605	62.302	1.00	27.93	A	O
ATOM	466	N	GLN	A	184	18.668	103.261	62.168	1.00	29.56	A	N
ATOM	467	CA	GLN	A	184	18.349	102.519	63.373	1.00	30.04	A	C
ATOM	468	CB	GLN	A	184	19.315	101.345	63.495	1.00	30.32	A	C
ATOM	469	CG	GLN	A	184	18.801	100.235	64.369	1.00	34.52	A	C
ATOM	470	CD	GLN	A	184	17.721	99.403	63.709	1.00	32.90	A	C
ATOM	471	OE1	GLN	A	184	16.988	98.695	64.388	1.00	36.44	A	O
ATOM	472	NE2	GLN	A	184	17.628	99.470	62.386	1.00	32.19	A	N
ATOM	473	C	GLN	A	184	18.335	103.318	64.679	1.00	31.00	A	C
ATOM	474	O	GLN	A	184	17.593	102.988	65.606	1.00	29.21	A	O
ATOM	475	N	SER	A	185	19.139	104.375	64.752	1.00	32.70	A	N
ATOM	476	CA	SER	A	185	19.219	105.179	65.968	1.00	33.38	A	C
ATOM	477	CB	SER	A	185	20.512	105.985	65.976	1.00	34.25	A	C
ATOM	478	OG	SER	A	185	20.402	107.001	64.996	1.00	35.32	A	O
ATOM	479	C	SER	A	185	18.051	106.134	66.192	1.00	34.71	A	C
ATOM	480	O	SER	A	185	17.989	106.797	67.221	1.00	34.82	A	O
ATOM	481	N	HIS	A	186	17.131	106.212	65.237	1.00	35.78	A	N
ATOM	482	CA	HIS	A	186	15.974	107.098	65.366	1.00	36.17	A	C
ATOM	483	CB	HIS	A	186	15.875	108.002	64.133	1.00	38.62	A	C
ATOM	484	CG	HIS	A	186	17.044	108.925	63.970	1.00	42.07	A	C
ATOM	485	CD2	HIS	A	186	17.816	109.557	64.886	1.00	42.75	A	C
ATOM	486	ND1	HIS	A	186	17.538	109.290	62.736	1.00	42.17	A	N
ATOM	487	CE1	HIS	A	186	18.566	110.104	62.899	1.00	42.82	A	C
ATOM	488	NE2	HIS	A	186	18.755	110.283	64.194	1.00	43.03	A	N
ATOM	489	C	HIS	A	186	14.673	106.310	65.545	1.00	35.02	A	C
ATOM	490	O	HIS	A	186	13.558	106.868	65.449	1.00	36.65	A	O
ATOM	491	N	LEU	A	187	14.796	105.011	65.793	1.00	31.62	A	N
ATOM	492	CA	LEU	A	187	13.631	104.161	65.994	1.00	29.84	A	C
ATOM	493	CB	LEU	A	187	13.791	102.828	65.253	1.00	28.15	A	C
ATOM	494	CG	LEU	A	187	13.577	102.778	63.743	1.00	28.01	A	C
ATOM	495	CD1	LEU	A	187	14.398	103.855	63.066	1.00	31.70	A	C
ATOM	496	CD2	LEU	A	187	13.973	101.410	63.226	1.00	25.23	A	C
ATOM	497	C	LEU	A	187	13.480	103.886	67.479	1.00	28.25	A	C
ATOM	498	O	LEU	A	187	14.397	103.359	68.110	1.00	28.90	A	O
ATOM	499	N	ALA	A	188	12.333	104.254	68.038	1.00	25.67	A	N
ATOM	500	CA	ALA	A	188	12.074	104.024	69.451	1.00	23.28	A	C
ATOM	501	CB	ALA	A	188	11.981	105.355	70.201	1.00	22.40	A	C
ATOM	502	C	ALA	A	188	10.782	103.241	69.612	1.00	21.56	A	C
ATOM	503	O	ALA	A	188	9.695	103.793	69.488	1.00	21.09	A	O
ATOM	504	N	HIS	A	189	10.906	101.944	69.859	1.00	21.04	A	N
ATOM	505	CA	HIS	A	189	9.736	101.088	70.048	1.00	22.71	A	C
ATOM	506	CB	HIS	A	189	9.299	100.458	68.720	1.00	22.11	A	C
ATOM	507	CG	HIS	A	189	7.961	99.784	68.774	1.00	23.56	A	C
ATOM	508	CD2	HIS	A	189	7.621	98.494	69.014	1.00	23.56	A	C
ATOM	509	ND1	HIS	A	189	6.775	100.456	68.562	1.00	26.00	A	N
ATOM	510	CE1	HIS	A	189	5.765	99.612	68.666	1.00	23.68	A	C
ATOM	511	NE2	HIS	A	189	6.251	98.414	68.941	1.00	25.80	A	N
ATOM	512	C	HIS	A	189	10.122	99.999	71.045	1.00	22.46	A	C
ATOM	513	O	HIS	A	189	11.254	99.509	71.041	1.00	22.66	A	O
ATOM	514	N	PRO	A	190	9.185	99.615	71.919	1.00	22.08	A	N
ATOM	515	CD	PRO	A	190	7.823	100.159	72.076	1.00	22.50	A	C
ATOM	516	CA	PRO	A	190	9.458	98.584	72.915	1.00	22.42	A	C
ATOM	517	CB	PRO	A	190	8.238	98.659	73.837	1.00	22.67	A	C
ATOM	518	CG	PRO	A	190	7.149	99.106	72.925	1.00	23.94	A	C
ATOM	519	C	PRO	A	190	9.688	97.190	72.341	1.00	23.17	A	C
ATOM	520	O	PRO	A	190	10.091	96.282	73.070	1.00	21.69	A	O
ATOM	521	N	ASN	A	191	9.445	97.015	71.043	1.00	21.27	A	N

	ATOM	522	CA	ASN	A	191	9.657	95.711	70.422	1.00	19.49	A C
	ATOM	523	CB	ASN	A	191	8.361	95.170	69.831	1.00	19.45	A C
	ATOM	524	CG	ASN	A	191	7.320	94.880	70.884	1.00	19.61	A C
	ATOM	525	OD1	ASN	A	191	7.495	93.995	71.715	1.00	22.06	A O
5	ATOM	526	ND2	ASN	A	191	6.227	95.628	70.855	1.00	20.03	A N
	ATOM	527	C	ASN	A	191	10.732	95.753	69.345	1.00	19.88	A C
	ATOM	528	O	ASN	A	191	10.813	94.857	68.497	1.00	19.36	A O
	ATOM	529	N	ILE	A	192	11.542	96.807	69.380	1.00	18.73	A N
	ATOM	530	CA	ILE	A	192	12.652	96.973	68.454	1.00	18.72	A C
10	ATOM	531	CB	ILE	A	192	12.412	98.160	67.491	1.00	18.58	A C
	ATOM	532	CG2	ILE	A	192	13.676	98.453	66.697	1.00	15.53	A C
	ATOM	533	CG1	ILE	A	192	11.252	97.824	66.543	1.00	20.81	A C
	ATOM	534	CD1	ILE	A	192	10.965	98.892	65.507	1.00	22.29	A C
	ATOM	535	C	ILE	A	192	13.904	97.224	69.300	1.00	19.43	A C
15	ATOM	536	O	ILE	A	192	13.909	98.111	70.157	1.00	21.71	A O
	ATOM	537	N	LEU	A	193	14.957	96.441	69.075	1.00	18.98	A N
	ATOM	538	CA	LEU	A	193	16.188	96.588	69.860	1.00	20.69	A C
	ATOM	539	CB	LEU	A	193	17.214	95.514	69.467	1.00	19.99	A C
	ATOM	540	CG	LEU	A	193	18.234	95.145	70.558	1.00	21.41	A C
20	ATOM	541	CD1	LEU	A	193	17.560	94.248	71.601	1.00	18.84	A C
	ATOM	542	CD2	LEU	A	193	19.431	94.424	69.942	1.00	20.29	A C
	ATOM	543	C	LEU	A	193	16.799	97.985	69.693	1.00	19.95	A C
	ATOM	544	O	LEU	A	193	17.020	98.455	68.578	1.00	21.40	A O
	ATOM	545	N	ARG	A	194	17.060	98.647	70.811	1.00	19.34	A N
25	ATOM	546	CA	ARG	A	194	17.628	99.988	70.805	1.00	18.88	A C
	ATOM	547	CB	ARG	A	194	17.376	100.662	72.154	1.00	23.30	A C
	ATOM	548	CG	ARG	A	194	16.092	101.460	72.259	1.00	29.13	A C
	ATOM	549	CD	ARG	A	194	16.164	102.728	71.425	1.00	36.10	A C
	ATOM	550	NE	ARG	A	194	15.089	103.659	71.763	1.00	41.78	A N
30	ATOM	551	CZ	ARG	A	194	14.999	104.308	72.922	1.00	44.56	A C
	ATOM	552	NH1	ARG	A	194	15.925	104.131	73.860	1.00	45.72	A N
	ATOM	553	NH2	ARG	A	194	13.983	105.132	73.147	1.00	45.18	A N
	ATOM	554	C	ARG	A	194	19.126	100.073	70.513	1.00	18.39	A C
	ATOM	555	O	ARG	A	194	19.919	99.292	71.031	1.00	15.95	A O
35	ATOM	556	N	LEU	A	195	19.493	101.035	69.673	1.00	18.46	A N
	ATOM	557	CA	LEU	A	195	20.887	101.311	69.355	1.00	22.13	A C
	ATOM	558	CB	LEU	A	195	21.056	101.650	67.869	1.00	23.02	A C
	ATOM	559	CG	LEU	A	195	22.400	101.369	67.180	1.00	25.45	A C
	ATOM	560	CD1	LEU	A	195	22.513	102.259	65.948	1.00	24.91	A C
40	ATOM	561	CD2	LEU	A	195	23.570	101.636	68.111	1.00	25.90	A C
	ATOM	562	C	LEU	A	195	21.116	102.573	70.196	1.00	22.63	A C
	ATOM	563	O	LEU	A	195	20.599	103.633	69.862	1.00	24.54	A O
	ATOM	564	N	TYR	A	196	21.851	102.456	71.294	1.00	22.66	A N
	ATOM	565	CA	TYR	A	196	22.095	103.605	72.168	1.00	23.33	A C
45	ATOM	566	CB	TYR	A	196	22.619	103.141	73.534	1.00	22.65	A C
	ATOM	567	CG	TYR	A	196	21.702	102.221	74.310	1.00	21.37	A C
	ATOM	568	CD1	TYR	A	196	22.190	101.040	74.879	1.00	22.83	A C
	ATOM	569	CE1	TYR	A	196	21.387	100.235	75.677	1.00	22.12	A C
	ATOM	570	CD2	TYR	A	196	20.379	102.565	74.551	1.00	22.29	A C
50	ATOM	571	CE2	TYR	A	196	19.561	101.765	75.348	1.00	23.98	A C
	ATOM	572	CZ	TYR	A	196	20.075	100.603	75.911	1.00	25.61	A C
	ATOM	573	OH	TYR	A	196	19.277	99.825	76.725	1.00	27.32	A O
	ATOM	574	C	TYR	A	196	23.088	104.603	71.574	1.00	23.97	A C
	ATOM	575	O	TYR	A	196	23.028	105.794	71.867	1.00	24.83	A O
55	ATOM	576	N	GLY	A	197	24.008	104.114	70.750	1.00	25.27	A N
	ATOM	577	CA	GLY	A	197	24.985	104.999	70.141	1.00	23.65	A C
	ATOM	578	C	GLY	A	197	26.091	104.230	69.457	1.00	24.59	A C
	ATOM	579	O	GLY	A	197	25.990	103.019	69.276	1.00	24.07	A O
	ATOM	580	N	TYR	A	198	27.147	104.934	69.070	1.00	26.73	A N
60	ATOM	581	CA	TYR	A	198	28.282	104.307	68.413	1.00	29.46	A C
	ATOM	582	CB	TYR	A	198	27.894	103.881	66.994	1.00	33.22	A C
	ATOM	583	CG	TYR	A	198	27.914	104.997	65.981	1.00	38.83	A C
	ATOM	584	CD1	TYR	A	198	29.029	105.197	65.165	1.00	40.36	A C
	ATOM	585	CE1	TYR	A	198	29.066	106.235	64.237	1.00	44.11	A C
65	ATOM	586	CD2	TYR	A	198	26.810	105.865	65.846	1.00	41.61	A C
	ATOM	587	CE2	TYR	A	198	26.856	106.912	64.917	1.00	44.45	A C
	ATOM	588	CZ	TYR	A	198	27.978	107.088	64.118	1.00	45.02	A C
	ATOM	589	OH	TYR	A	198	28.016	108.112	63.195	1.00	48.52	A O
	ATOM	590	C	TYR	A	198	29.462	105.272	68.366	1.00	29.09	A C
70	ATOM	591	O	TYR	A	198	29.286	106.475	68.477	1.00	28.17	A O
	ATOM	592	N	PHE	A	199	30.664	104.729	68.218	1.00	30.25	A N
	ATOM	593	CA	PHE	A	199	31.880	105.533	68.134	1.00	31.17	A C

ATOM	594	CB	PHE	A	199	32.356	105.961	69.529	1.00	29.63	A	C
ATOM	595	CG	PHE	A	199	32.650	104.819	70.462	1.00	28.60	A	C
ATOM	596	CD1	PHE	A	199	33.957	104.372	70.648	1.00	29.19	A	C
ATOM	597	CD2	PHE	A	199	31.624	104.210	71.181	1.00	27.35	A	C
ATOM	598	CE1	PHE	A	199	34.242	103.335	71.541	1.00	28.83	A	C
ATOM	599	CE2	PHE	A	199	31.894	103.171	72.076	1.00	28.14	A	C
ATOM	600	CZ	PHE	A	199	33.208	102.732	72.258	1.00	28.52	A	C
ATOM	601	C	PHE	A	199	32.946	104.707	67.435	1.00	32.80	A	C
ATOM	602	O	PHE	A	199	32.689	103.574	67.032	1.00	31.66	A	O
ATOM	603	N	HIS	A	200	34.137	105.269	67.277	1.00	35.04	A	N
ATOM	604	CA	HIS	A	200	35.204	104.542	66.604	1.00	37.23	A	C
ATOM	605	CB	HIS	A	200	35.033	104.644	65.082	1.00	38.99	A	C
ATOM	606	CG	HIS	A	200	35.193	106.036	64.552	1.00	41.96	A	C
ATOM	607	CD2	HIS	A	200	36.210	106.620	63.875	1.00	43.26	A	C
ATOM	608	ND1	HIS	A	200	34.257	107.027	64.763	1.00	44.18	A	N
ATOM	609	CE1	HIS	A	200	34.691	108.160	64.240	1.00	43.73	A	C
ATOM	610	NE2	HIS	A	200	35.875	107.940	63.697	1.00	43.65	A	N
ATOM	611	C	HIS	A	200	36.570	105.083	66.987	1.00	36.48	A	C
ATOM	612	O	HIS	A	200	36.679	106.156	67.574	1.00	37.25	A	O
ATOM	613	N	ASP	A	201	37.607	104.315	66.673	1.00	36.48	A	N
ATOM	614	CA	ASP	A	201	38.981	104.730	66.930	1.00	35.68	A	C
ATOM	615	CB	ASP	A	201	39.662	103.861	68.007	1.00	34.18	A	C
ATOM	616	CG	ASP	A	201	39.533	102.371	67.745	1.00	33.78	A	C
ATOM	617	OD1	ASP	A	201	39.597	101.946	66.574	1.00	33.96	A	O
ATOM	618	OD2	ASP	A	201	39.386	101.616	68.731	1.00	35.77	A	O
ATOM	619	C	ASP	A	201	39.717	104.633	65.599	1.00	35.73	A	C
ATOM	620	O	ASP	A	201	39.136	104.924	64.556	1.00	36.16	A	O
ATOM	621	N	ALA	A	202	40.977	104.215	65.614	1.00	36.60	A	N
ATOM	622	CA	ALA	A	202	41.738	104.124	64.372	1.00	35.67	A	C
ATOM	623	CB	ALA	A	202	43.228	104.205	64.676	1.00	34.98	A	C
ATOM	624	C	ALA	A	202	41.444	102.881	63.530	1.00	36.02	A	C
ATOM	625	O	ALA	A	202	41.396	102.960	62.302	1.00	36.18	A	O
ATOM	626	N	ALA	A	203	41.234	101.741	64.182	1.00	35.91	A	N
ATOM	627	CA	ALA	A	203	40.983	100.499	63.455	1.00	35.99	A	C
ATOM	628	CB	ALA	A	203	42.056	99.474	63.822	1.00	35.92	A	C
ATOM	629	C	ALA	A	203	39.599	99.881	63.642	1.00	35.06	A	C
ATOM	630	O	ALA	A	203	39.167	99.058	62.833	1.00	35.70	A	O
ATOM	631	N	ARG	A	204	38.896	100.275	64.697	1.00	34.43	A	N
ATOM	632	CA	ARG	A	204	37.580	99.700	64.962	1.00	32.43	A	C
ATOM	633	CB	ARG	A	204	37.648	98.895	66.267	1.00	32.75	A	C
ATOM	634	CG	ARG	A	204	38.506	97.632	66.175	1.00	35.06	A	C
ATOM	635	CD	ARG	A	204	39.131	97.280	67.516	1.00	35.42	A	C
ATOM	636	NE	ARG	A	204	40.124	98.281	67.891	1.00	39.37	A	N
ATOM	637	CZ	ARG	A	204	40.829	98.271	69.020	1.00	39.97	A	C
ATOM	638	NH1	ARG	A	204	40.664	97.303	69.915	1.00	41.24	A	N
ATOM	639	NH2	ARG	A	204	41.691	99.249	69.259	1.00	42.09	A	N
ATOM	640	C	ARG	A	204	36.397	100.675	65.019	1.00	29.51	A	C
ATOM	641	O	ARG	A	204	36.563	101.873	65.235	1.00	27.71	A	O
ATOM	642	N	VAL	A	205	35.203	100.124	64.810	1.00	27.67	A	N
ATOM	643	CA	VAL	A	205	33.945	100.864	64.873	1.00	26.35	A	C
ATOM	644	CB	VAL	A	205	33.203	100.843	63.514	1.00	27.17	A	C
ATOM	645	CG1	VAL	A	205	31.863	101.555	63.639	1.00	28.86	A	C
ATOM	646	CG2	VAL	A	205	34.049	101.521	62.446	1.00	28.26	A	C
ATOM	647	C	VAL	A	205	33.103	100.127	65.919	1.00	24.01	A	C
ATOM	648	O	VAL	A	205	32.992	98.892	65.876	1.00	22.92	A	O
ATOM	649	N	TYR	A	206	32.516	100.868	66.852	1.00	22.11	A	N
ATOM	650	CA	TYR	A	206	31.723	100.254	67.919	1.00	21.58	A	C
ATOM	651	CB	TYR	A	206	32.341	100.574	69.286	1.00	24.51	A	C
ATOM	652	CG	TYR	A	206	33.832	100.308	69.398	1.00	28.74	A	C
ATOM	653	CD1	TYR	A	206	34.768	101.282	69.043	1.00	30.43	A	C
ATOM	654	CE1	TYR	A	206	36.148	101.040	69.156	1.00	33.31	A	C
ATOM	655	CD2	TYR	A	206	34.304	99.084	69.862	1.00	30.70	A	C
ATOM	656	CE2	TYR	A	206	35.672	98.832	69.974	1.00	33.27	A	C
ATOM	657	CZ	TYR	A	206	36.587	99.810	69.624	1.00	33.23	A	C
ATOM	658	OH	TYR	A	206	37.934	99.555	69.755	1.00	33.76	A	O
ATOM	659	C	TYR	A	206	30.245	100.650	67.964	1.00	20.45	A	C
ATOM	660	O	TYR	A	206	29.898	101.825	67.828	1.00	20.51	A	O
ATOM	661	N	LEU	A	207	29.385	99.659	68.179	1.00	19.23	A	N
ATOM	662	CA	LEU	A	207	27.943	99.883	68.290	1.00	20.53	A	C
ATOM	663	CB	LEU	A	207	27.183	99.001	67.288	1.00	21.53	A	C
ATOM	664	CG	LEU	A	207	27.574	99.160	65.814	1.00	21.15	A	C
ATOM	665	CD1	LEU	A	207	26.675	98.309	64.950	1.00	23.10	A	C

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ATOM    666  CD2 LEU A 207      27.462 100.624  65.412  1.00 23.96           A    C
ATOM    667  C   LEU A 207      27.495  99.542  69.712  1.00 20.27           A    C
ATOM    668  O   LEU A 207      27.760  98.443  70.204  1.00 22.20           A    O
ATOM    669  N   ILE A 208      26.825 100.480  70.375  1.00 18.68           A    N
ATOM    670  CA  ILE A 208      26.350 100.256  71.736  1.00 18.33           A    C
ATOM    671  CB  ILE A 208      26.514 101.518  72.599  1.00 17.78           A    C
ATOM    672  CG2 ILE A 208      26.331 101.161  74.075  1.00 18.29           A    C
ATOM    673  CG1 ILE A 208      27.896 102.138  72.365  1.00 21.18           A    C
ATOM    674  CD1 ILE A 208      28.109 103.468  73.086  1.00 19.74           A    C
ATOM    675  C   ILE A 208      24.864  99.895  71.650  1.00 19.02           A    C
ATOM    676  O   ILE A 208      24.025 100.749  71.332  1.00 20.96           A    O
ATOM    677  N   LEU A 209      24.554  98.639  71.963  1.00 18.23           A    N
ATOM    678  CA  LEU A 209      23.200  98.100  71.868  1.00 17.67           A    C
ATOM    679  CB  LEU A 209      23.216  96.893  70.941  1.00 17.32           A    C
ATOM    680  CG  LEU A 209      23.871  97.022  69.564  1.00 19.38           A    C
ATOM    681  CD1 LEU A 209      24.381  95.647  69.117  1.00 20.09           A    C
ATOM    682  CD2 LEU A 209      22.877  97.587  68.571  1.00 19.54           A    C
ATOM    683  C   LEU A 209      22.519  97.668  73.160  1.00 19.32           A    C
ATOM    684  O   LEU A 209      23.169  97.322  74.149  1.00 18.62           A    O
ATOM    685  N   GLU A 210      21.190  97.682  73.124  1.00 17.29           A    N
ATOM    686  CA  GLU A 210      20.373  97.235  74.240  1.00 17.08           A    C
ATOM    687  CB  GLU A 210      18.892  97.490  73.922  1.00 17.25           A    C
ATOM    688  CG  GLU A 210      17.915  97.005  74.971  1.00 14.08           A    C
ATOM    689  CD  GLU A 210      16.466  97.056  74.493  1.00 16.64           A    C
ATOM    690  OE1 GLU A 210      15.579  96.672  75.275  1.00 16.48           A    O
ATOM    691  OE2 GLU A 210      16.210  97.470  73.338  1.00 18.70           A    O
ATOM    692  C   GLU A 210      20.623  95.724  74.369  1.00 17.70           A    C
ATOM    693  O   GLU A 210      20.722  95.018  73.367  1.00 16.33           A    O
ATOM    694  N   TYR A 211      20.737  95.230  75.596  1.00 18.29           A    N
ATOM    695  CA  TYR A 211      20.992  93.811  75.817  1.00 18.22           A    C
ATOM    696  CB  TYR A 211      21.889  93.644  77.045  1.00 21.03           A    C
ATOM    697  CG  TYR A 211      22.150  92.216  77.474  1.00 21.77           A    C
ATOM    698  CD1 TYR A 211      22.898  91.347  76.681  1.00 22.50           A    C
ATOM    699  CE1 TYR A 211      23.160  90.036  77.103  1.00 23.40           A    C
ATOM    700  CD2 TYR A 211      21.671  91.743  78.696  1.00 22.56           A    C
ATOM    701  CE2 TYR A 211      21.928  90.443  79.124  1.00 21.84           A    C
ATOM    702  CZ  TYR A 211      22.666  89.598  78.328  1.00 22.93           A    C
ATOM    703  OH  TYR A 211      22.902  88.314  78.757  1.00 24.56           A    O
ATOM    704  C   TYR A 211      19.704  93.011  75.996  1.00 17.77           A    C
ATOM    705  O   TYR A 211      18.791  93.444  76.694  1.00 16.95           A    O
ATOM    706  N   ALA A 212      19.642  91.845  75.353  1.00 18.77           A    N
ATOM    707  CA  ALA A 212      18.477  90.952  75.439  1.00 18.90           A    C
ATOM    708  CB  ALA A 212      18.090  90.485  74.040  1.00 16.75           A    C
ATOM    709  C   ALA A 212      18.873  89.755  76.325  1.00 19.85           A    C
ATOM    710  O   ALA A 212      19.515  88.837  75.872  1.00 20.40           A    O
ATOM    711  N   PRO A 213      18.444  89.757  77.602  1.00 21.83           A    N
ATOM    712  CD  PRO A 213      17.600  90.806  78.190  1.00 22.17           A    C
ATOM    713  CA  PRO A 213      18.727  88.726  78.609  1.00 22.10           A    C
ATOM    714  CB  PRO A 213      18.026  89.258  79.865  1.00 23.45           A    C
ATOM    715  CG  PRO A 213      17.976  90.713  79.651  1.00 24.12           A    C
ATOM    716  C   PRO A 213      18.318  87.295  78.320  1.00 22.31           A    C
ATOM    717  O   PRO A 213      19.019  86.360  78.703  1.00 22.54           A    O
ATOM    718  N   LEU A 214      17.184  87.111  77.656  1.00 22.59           A    N
ATOM    719  CA  LEU A 214      16.715  85.765  77.375  1.00 20.79           A    C
ATOM    720  CB  LEU A 214      15.181  85.716  77.499  1.00 21.06           A    C
ATOM    721  CG  LEU A 214      14.680  85.611  78.950  1.00 22.27           A    C
ATOM    722  CD1 LEU A 214      15.249  86.752  79.769  1.00 25.21           A    C
ATOM    723  CD2 LEU A 214      13.160  85.633  79.001  1.00 21.90           A    C
ATOM    724  C   LEU A 214      17.189  85.117  76.075  1.00 20.41           A    C
ATOM    725  O   LEU A 214      16.846  83.975  75.805  1.00 21.99           A    O
ATOM    726  N   GLY A 215      17.986  85.823  75.276  1.00 20.34           A    N
ATOM    727  CA  GLY A 215      18.503  85.227  74.047  1.00 22.43           A    C
ATOM    728  C   GLY A 215      17.611  85.190  72.813  1.00 21.59           A    C
ATOM    729  O   GLY A 215      16.679  85.976  72.696  1.00 23.24           A    O
ATOM    730  N   THR A 216      17.892  84.273  71.889  1.00 22.02           A    N
ATOM    731  CA  THR A 216      17.112  84.172  70.652  1.00 23.73           A    C
ATOM    732  CB  THR A 216      17.960  83.626  69.487  1.00 24.78           A    C
ATOM    733  OG1 THR A 216      18.233  82.238  69.706  1.00 25.51           A    O
ATOM    734  CG2 THR A 216      19.270  84.397  69.369  1.00 25.01           A    C
ATOM    735  C   THR A 216      15.851  83.314  70.720  1.00 23.31           A    C
ATOM    736  O   THR A 216      15.750  82.382  71.513  1.00 21.80           A    O
ATOM    737  N   VAL A 217      14.886  83.645  69.867  1.00 25.09           A    N
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ATOM	738	CA	VAL	A	217	13.626	82.904	69.797	1.00	25.79	A C
ATOM	739	CB	VAL	A	217	12.604	83.633	68.902	1.00	23.02	A C
ATOM	740	CG1	VAL	A	217	11.368	82.773	68.703	1.00	24.17	A C
ATOM	741	CG2	VAL	A	217	12.234	84.961	69.533	1.00	22.94	A C
ATOM	742	C	VAL	A	217	13.921	81.530	69.196	1.00	26.14	A C
ATOM	743	O	VAL	A	217	13.278	80.534	69.525	1.00	25.55	A O
ATOM	744	N	TYR	A	218	14.909	81.501	68.314	1.00	26.45	A N
ATOM	745	CA	TYR	A	218	15.327	80.283	67.655	1.00	30.04	A C
ATOM	746	CB	TYR	A	218	16.464	80.624	66.690	1.00	34.58	A C
ATOM	747	CG	TYR	A	218	17.201	79.443	66.113	1.00	40.28	A C
ATOM	748	CD1	TYR	A	218	18.240	78.834	66.818	1.00	43.24	A C
ATOM	749	CE1	TYR	A	218	18.945	77.765	66.277	1.00	44.89	A C
ATOM	750	CD2	TYR	A	218	16.882	78.949	64.854	1.00	42.24	A C
ATOM	751	CE2	TYR	A	218	17.579	77.879	64.304	1.00	44.73	A C
ATOM	752	CZ	TYR	A	218	18.608	77.292	65.019	1.00	46.29	A C
ATOM	753	OH	TYR	A	218	19.304	76.235	64.475	1.00	48.71	A O
ATOM	754	C	TYR	A	218	15.759	79.241	68.684	1.00	30.04	A C
ATOM	755	O	TYR	A	218	15.383	78.075	68.607	1.00	29.65	A O
ATOM	756	N	ARG	A	219	16.534	79.675	69.668	1.00	31.08	A N
ATOM	757	CA	ARG	A	219	17.011	78.778	70.702	1.00	30.24	A C
ATOM	758	CB	ARG	A	219	18.047	79.502	71.555	1.00	34.57	A C
ATOM	759	CG	ARG	A	219	18.660	78.657	72.634	1.00	39.81	A C
ATOM	760	CD	ARG	A	219	19.723	79.443	73.374	1.00	45.90	A C
ATOM	761	NE	ARG	A	219	20.255	78.683	74.501	1.00	51.60	A N
ATOM	762	CZ	ARG	A	219	21.250	79.097	75.276	1.00	52.82	A C
ATOM	763	NH1	ARG	A	219	21.826	80.273	75.041	1.00	53.30	A N
ATOM	764	NH2	ARG	A	219	21.658	78.338	76.289	1.00	53.23	A N
ATOM	765	C	ARG	A	219	15.855	78.267	71.556	1.00	29.44	A C
ATOM	766	O	ARG	A	219	15.829	77.101	71.941	1.00	28.48	A O
ATOM	767	N	GLU	A	220	14.892	79.138	71.840	1.00	29.18	A N
ATOM	768	CA	GLU	A	220	13.721	78.765	72.627	1.00	29.90	A C
ATOM	769	CB	GLU	A	220	12.873	80.011	72.924	1.00	30.93	A C
ATOM	770	CG	GLU	A	220	11.570	79.737	73.653	1.00	35.19	A C
ATOM	771	CD	GLU	A	220	10.684	80.975	73.765	1.00	38.55	A C
ATOM	772	OE1	GLU	A	220	10.619	81.754	72.789	1.00	41.41	A O
ATOM	773	OE2	GLU	A	220	10.036	81.165	74.816	1.00	38.75	A O
ATOM	774	C	GLU	A	220	12.890	77.730	71.852	1.00	29.28	A C
ATOM	775	O	GLU	A	220	12.319	76.813	72.434	1.00	29.27	A O
ATOM	776	N	LEU	A	221	12.846	77.882	70.533	1.00	29.01	A N
ATOM	777	CA	LEU	A	221	12.095	76.981	69.661	1.00	29.41	A C
ATOM	778	CB	LEU	A	221	12.087	77.547	68.234	1.00	29.75	A C
ATOM	779	CG	LEU	A	221	11.135	76.947	67.198	1.00	27.34	A C
ATOM	780	CD1	LEU	A	221	9.691	77.040	67.681	1.00	26.36	A C
ATOM	781	CD2	LEU	A	221	11.298	77.707	65.902	1.00	28.29	A C
ATOM	782	C	LEU	A	221	12.691	75.570	69.655	1.00	31.02	A C
ATOM	783	O	LEU	A	221	11.958	74.579	69.659	1.00	30.54	A O
ATOM	784	N	GLN	A	222	14.022	75.487	69.636	1.00	32.15	A N
ATOM	785	CA	GLN	A	222	14.718	74.204	69.644	1.00	33.38	A C
ATOM	786	CB	GLN	A	222	16.224	74.405	69.478	1.00	36.12	A C
ATOM	787	CG	GLN	A	222	16.624	75.120	68.206	1.00	40.81	A C
ATOM	788	CD	GLN	A	222	18.126	75.279	68.092	1.00	44.96	A C
ATOM	789	OE1	GLN	A	222	18.787	75.722	69.033	1.00	46.46	A O
ATOM	790	NE2	GLN	A	222	18.675	74.924	66.933	1.00	47.81	A N
ATOM	791	C	GLN	A	222	14.467	73.437	70.937	1.00	33.08	A C
ATOM	792	O	GLN	A	222	14.435	72.212	70.933	1.00	33.65	A O
ATOM	793	N	LYS	A	223	14.288	74.160	72.038	1.00	32.99	A N
ATOM	794	CA	LYS	A	223	14.045	73.539	73.336	1.00	32.56	A C
ATOM	795	CB	LYS	A	223	14.314	74.541	74.464	1.00	35.07	A C
ATOM	796	CG	LYS	A	223	15.780	74.660	74.873	1.00	38.94	A C
ATOM	797	CD	LYS	A	223	16.682	74.938	73.680	1.00	42.58	A C
ATOM	798	CE	LYS	A	223	18.143	75.049	74.084	1.00	45.75	A C
ATOM	799	NZ	LYS	A	223	19.012	75.377	72.910	1.00	47.32	A N
ATOM	800	C	LYS	A	223	12.629	72.992	73.480	1.00	31.92	A C
ATOM	801	O	LYS	A	223	12.444	71.840	73.869	1.00	31.63	A O
ATOM	802	N	LEU	A	224	11.632	73.815	73.159	1.00	29.58	A N
ATOM	803	CA	LEU	A	224	10.235	73.413	73.272	1.00	27.04	A C
ATOM	804	CB	LEU	A	224	9.355	74.651	73.488	1.00	27.41	A C
ATOM	805	CG	LEU	A	224	9.626	75.554	74.703	1.00	26.07	A C
ATOM	806	CD1	LEU	A	224	8.545	76.626	74.805	1.00	23.48	A C
ATOM	807	CD2	LEU	A	224	9.632	74.717	75.968	1.00	26.95	A C
ATOM	808	C	LEU	A	224	9.698	72.613	72.080	1.00	26.87	A C
ATOM	809	O	LEU	A	224	8.653	71.977	72.187	1.00	27.46	A O

ATOM	810	N	SER	A	225	10.410	72.650	70.954	1.00	26.55	A	N
ATOM	811	CA	SER	A	225	10.009	71.944	69.730	1.00	28.34	A	C
ATOM	812	CB	SER	A	225	9.473	70.549	70.062	1.00	30.23	A	C
ATOM	813	OG	SER	A	225	9.605	69.698	68.941	1.00	33.93	A	O
ATOM	814	C	SER	A	225	8.964	72.732	68.920	1.00	26.55	A	C
ATOM	815	O	SER	A	225	9.046	72.810	67.697	1.00	26.63	A	O
ATOM	816	N	LYS	A	226	7.977	73.296	69.607	1.00	25.84	A	N
ATOM	817	CA	LYS	A	226	6.958	74.129	68.976	1.00	25.88	A	C
ATOM	818	CB	LYS	A	226	6.012	73.304	68.087	1.00	28.21	A	C
ATOM	819	CG	LYS	A	226	5.184	72.259	68.790	1.00	28.88	A	C
ATOM	820	CD	LYS	A	226	4.409	71.443	67.770	1.00	34.11	A	C
ATOM	821	CE	LYS	A	226	3.483	70.427	68.435	1.00	34.70	A	C
ATOM	822	NZ	LYS	A	226	4.240	69.444	69.261	1.00	37.81	A	N
ATOM	823	C	LYS	A	226	6.191	74.851	70.073	1.00	25.27	A	C
ATOM	824	O	LYS	A	226	6.124	74.373	71.202	1.00	26.71	A	O
ATOM	825	N	PHE	A	227	5.637	76.016	69.749	1.00	24.65	A	N
ATOM	826	CA	PHE	A	227	4.891	76.808	70.722	1.00	22.54	A	C
ATOM	827	CB	PHE	A	227	5.085	78.312	70.463	1.00	23.44	A	C
ATOM	828	CG	PHE	A	227	6.527	78.753	70.359	1.00	20.95	A	C
ATOM	829	CD1	PHE	A	227	7.523	78.135	71.106	1.00	21.88	A	C
ATOM	830	CD2	PHE	A	227	6.868	79.847	69.561	1.00	19.95	A	C
ATOM	831	CE1	PHE	A	227	8.850	78.606	71.065	1.00	23.78	A	C
ATOM	832	CE2	PHE	A	227	8.183	80.326	69.511	1.00	21.33	A	C
ATOM	833	CZ	PHE	A	227	9.176	79.706	70.265	1.00	21.20	A	C
ATOM	834	C	PHE	A	227	3.397	76.514	70.673	1.00	22.04	A	C
ATOM	835	O	PHE	A	227	2.882	76.035	69.660	1.00	21.17	A	O
ATOM	836	N	ASP	A	228	2.707	76.813	71.768	1.00	19.93	A	N
ATOM	837	CA	ASP	A	228	1.269	76.617	71.842	1.00	21.17	A	C
ATOM	838	CB	ASP	A	228	0.840	76.388	73.294	1.00	22.28	A	C
ATOM	839	CG	ASP	A	228	1.204	77.547	74.203	1.00	24.14	A	C
ATOM	840	OD1	ASP	A	228	1.715	77.288	75.307	1.00	25.83	A	O
ATOM	841	OD2	ASP	A	228	0.968	78.718	73.829	1.00	24.66	A	O
ATOM	842	C	ASP	A	228	0.607	77.876	71.259	1.00	21.29	A	C
ATOM	843	O	ASP	A	228	1.287	78.878	70.977	1.00	20.58	A	O
ATOM	844	N	GLU	A	229	-0.707	77.829	71.086	1.00	19.93	A	N
ATOM	845	CA	GLU	A	229	-1.441	78.947	70.498	1.00	20.43	A	C
ATOM	846	CB	GLU	A	229	-2.919	78.586	70.333	1.00	22.25	A	C
ATOM	847	CG	GLU	A	229	-3.177	77.435	69.383	1.00	22.96	A	C
ATOM	848	CD	GLU	A	229	-4.657	77.151	69.227	1.00	23.72	A	C
ATOM	849	OE1	GLU	A	229	-5.276	76.655	70.185	1.00	27.47	A	O
ATOM	850	OE2	GLU	A	229	-5.203	77.437	68.152	1.00	23.78	A	O
ATOM	851	C	GLU	A	229	-1.330	80.270	71.237	1.00	20.15	A	C
ATOM	852	O	GLU	A	229	-1.247	81.320	70.598	1.00	19.16	A	O
ATOM	853	N	GLN	A	230	-1.337	80.238	72.569	1.00	17.98	A	N
ATOM	854	CA	GLN	A	230	-1.233	81.480	73.319	1.00	17.46	A	C
ATOM	855	CB	GLN	A	230	-1.412	81.246	74.833	1.00	16.42	A	C
ATOM	856	CG	GLN	A	230	-1.448	82.560	75.641	1.00	18.34	A	C
ATOM	857	CD	GLN	A	230	-1.683	82.377	77.140	1.00	18.98	A	C
ATOM	858	OE1	GLN	A	230	-0.744	82.430	77.933	1.00	21.19	A	O
ATOM	859	NE2	GLN	A	230	-2.932	82.167	77.529	1.00	16.82	A	N
ATOM	860	C	GLN	A	230	0.107	82.173	73.040	1.00	16.75	A	C
ATOM	861	O	GLN	A	230	0.136	83.359	72.679	1.00	17.29	A	O
ATOM	862	N	ARG	A	231	1.210	81.443	73.179	1.00	14.85	A	N
ATOM	863	CA	ARG	A	231	2.519	82.045	72.939	1.00	16.59	A	C
ATOM	864	CB	ARG	A	231	3.657	81.051	73.227	1.00	18.36	A	C
ATOM	865	CG	ARG	A	231	5.042	81.728	73.190	1.00	22.57	A	C
ATOM	866	CD	ARG	A	231	6.185	80.747	73.258	1.00	27.11	A	C
ATOM	867	NE	ARG	A	231	6.191	79.991	74.503	1.00	33.40	A	N
ATOM	868	CZ	ARG	A	231	6.654	80.446	75.664	1.00	35.76	A	C
ATOM	869	NH1	ARG	A	231	6.605	79.675	76.738	1.00	36.21	A	N
ATOM	870	NH2	ARG	A	231	7.176	81.660	75.752	1.00	38.74	A	N
ATOM	871	C	ARG	A	231	2.671	82.581	71.513	1.00	14.93	A	C
ATOM	872	O	ARG	A	231	3.151	83.700	71.311	1.00	14.16	A	O
ATOM	873	N	THR	A	232	2.276	81.776	70.531	1.00	15.57	A	N
ATOM	874	CA	THR	A	232	2.366	82.160	69.121	1.00	17.08	A	C
ATOM	875	CB	THR	A	232	1.859	81.030	68.188	1.00	18.02	A	C
ATOM	876	OG1	THR	A	232	2.656	79.856	68.382	1.00	18.40	A	O
ATOM	877	CG2	THR	A	232	1.953	81.451	66.718	1.00	15.83	A	C
ATOM	878	C	THR	A	232	1.553	83.420	68.821	1.00	17.13	A	C
ATOM	879	O	THR	A	232	2.061	84.359	68.204	1.00	18.70	A	O
ATOM	880	N	ALA	A	233	0.296	83.433	69.258	1.00	16.14	A	N
ATOM	881	CA	ALA	A	233	-0.590	84.568	69.025	1.00	16.30	A	C

ATOM	882	CB	ALA	A	233	-1.982	84.246	69.529	1.00	16.62	A	C
ATOM	883	C	ALA	A	233	-0.076	85.846	69.687	1.00	17.07	A	C
ATOM	884	O	ALA	A	233	-0.259	86.944	69.166	1.00	16.10	A	O
ATOM	885	N	THR	A	234	0.552	85.699	70.849	1.00	17.52	A	N
ATOM	886	CA	THR	A	234	1.092	86.845	71.552	1.00	16.78	A	C
ATOM	887	CB	THR	A	234	1.494	86.467	73.014	1.00	17.54	A	C
ATOM	888	OG1	THR	A	234	0.314	86.125	73.759	1.00	12.72	A	O
ATOM	889	CG2	THR	A	234	2.184	87.633	73.706	1.00	17.21	A	C
ATOM	890	C	THR	A	234	2.297	87.362	70.766	1.00	16.02	A	C
ATOM	891	O	THR	A	234	2.471	88.564	70.621	1.00	18.24	A	O
ATOM	892	N	TYR	A	235	3.116	86.459	70.239	1.00	15.74	A	N
ATOM	893	CA	TYR	A	235	4.275	86.879	69.456	1.00	18.00	A	C
ATOM	894	CB	TYR	A	235	5.180	85.694	69.117	1.00	18.40	A	C
ATOM	895	CG	TYR	A	235	6.016	85.167	70.264	1.00	22.59	A	C
ATOM	896	CD1	TYR	A	235	6.142	85.880	71.459	1.00	19.60	A	C
ATOM	897	CE1	TYR	A	235	6.943	85.413	72.490	1.00	23.79	A	C
ATOM	898	CD2	TYR	A	235	6.718	83.968	70.133	1.00	22.03	A	C
ATOM	899	CE2	TYR	A	235	7.530	83.492	71.158	1.00	25.06	A	C
ATOM	900	CZ	TYR	A	235	7.639	84.217	72.331	1.00	24.79	A	C
ATOM	901	OH	TYR	A	235	8.449	83.748	73.332	1.00	27.52	A	O
ATOM	902	C	TYR	A	235	3.882	87.574	68.148	1.00	17.48	A	C
ATOM	903	O	TYR	A	235	4.498	88.570	67.760	1.00	18.14	A	O
ATOM	904	N	ILE	A	236	2.869	87.050	67.463	1.00	15.10	A	N
ATOM	905	CA	ILE	A	236	2.443	87.655	66.207	1.00	15.95	A	C
ATOM	906	CB	ILE	A	236	1.374	86.784	65.505	1.00	15.91	A	C
ATOM	907	CG2	ILE	A	236	0.944	87.425	64.184	1.00	14.22	A	C
ATOM	908	CG1	ILE	A	236	1.950	85.393	65.225	1.00	13.58	A	C
ATOM	909	CD1	ILE	A	236	3.140	85.396	64.289	1.00	15.33	A	C
ATOM	910	C	ILE	A	236	1.905	89.070	66.425	1.00	16.93	A	C
ATOM	911	O	ILE	A	236	2.064	89.935	65.560	1.00	16.24	A	O
ATOM	912	N	THR	A	237	1.281	89.301	67.584	1.00	18.11	A	N
ATOM	913	CA	THR	A	237	0.727	90.613	67.937	1.00	19.28	A	C
ATOM	914	CB	THR	A	237	-0.107	90.545	69.255	1.00	22.99	A	C
ATOM	915	OG1	THR	A	237	-1.306	89.787	69.035	1.00	23.64	A	O
ATOM	916	CG2	THR	A	237	-0.470	91.953	69.741	1.00	21.39	A	C
ATOM	917	C	THR	A	237	1.863	91.610	68.152	1.00	19.31	A	C
ATOM	918	O	THR	A	237	1.787	92.763	67.726	1.00	20.31	A	O
ATOM	919	N	GLU	A	238	2.912	91.164	68.836	1.00	18.54	A	N
ATOM	920	CA	GLU	A	238	4.063	92.011	69.097	1.00	18.15	A	C
ATOM	921	CB	GLU	A	238	5.052	91.280	70.025	1.00	20.31	A	C
ATOM	922	CG	GLU	A	238	4.484	91.396	71.511	1.00	23.11	A	C
ATOM	923	CD	GLU	A	238	5.394	90.392	72.410	1.00	24.67	A	C
ATOM	924	OE1	GLU	A	238	6.516	89.946	72.079	1.00	24.03	A	O
ATOM	925	OE2	GLU	A	238	4.825	90.057	73.473	1.00	28.40	A	O
ATOM	926	C	GLU	A	238	4.746	92.432	67.794	1.00	17.67	A	C
ATOM	927	O	GLU	A	238	5.101	93.601	67.629	1.00	16.64	A	O
ATOM	928	N	LEU	A	239	4.917	91.487	66.869	1.00	18.93	A	N
ATOM	929	CA	LEU	A	239	5.555	91.769	65.573	1.00	19.50	A	C
ATOM	930	CB	LEU	A	239	5.822	90.469	64.813	1.00	18.18	A	C
ATOM	931	CG	LEU	A	239	6.841	89.501	65.407	1.00	23.44	A	C
ATOM	932	CD1	LEU	A	239	6.766	88.159	64.674	1.00	22.23	A	C
ATOM	933	CD2	LEU	A	239	8.236	90.107	65.314	1.00	21.26	A	C
ATOM	934	C	LEU	A	239	4.727	92.703	64.675	1.00	19.61	A	C
ATOM	935	O	LEU	A	239	5.279	93.583	64.024	1.00	17.80	A	O
ATOM	936	N	ALA	A	240	3.412	92.502	64.631	1.00	18.94	A	N
ATOM	937	CA	ALA	A	240	2.548	93.351	63.802	1.00	19.51	A	C
ATOM	938	CB	ALA	A	240	1.079	92.853	63.841	1.00	18.09	A	C
ATOM	939	C	ALA	A	240	2.633	94.787	64.288	1.00	18.99	A	C
ATOM	940	O	ALA	A	240	2.721	95.706	63.482	1.00	22.48	A	O
ATOM	941	N	ASN	A	241	2.610	94.992	65.603	1.00	21.18	A	N
ATOM	942	CA	ASN	A	241	2.736	96.347	66.135	1.00	21.65	A	C
ATOM	943	CB	ASN	A	241	2.687	96.365	67.663	1.00	23.20	A	C
ATOM	944	CG	ASN	A	241	1.299	96.153	68.203	1.00	24.44	A	C
ATOM	945	OD1	ASN	A	241	0.325	96.621	67.626	1.00	27.47	A	O
ATOM	946	ND2	ASN	A	241	1.189	95.462	69.326	1.00	27.36	A	N
ATOM	947	C	ASN	A	241	4.069	96.935	65.685	1.00	22.55	A	C
ATOM	948	O	ASN	A	241	4.111	98.035	65.129	1.00	24.99	A	O
ATOM	949	N	ALA	A	242	5.159	96.200	65.909	1.00	21.61	A	N
ATOM	950	CA	ALA	A	242	6.483	96.684	65.525	1.00	20.55	A	C
ATOM	951	CB	ALA	A	242	7.557	95.687	65.959	1.00	20.38	A	C
ATOM	952	C	ALA	A	242	6.607	96.967	64.026	1.00	21.10	A	C
ATOM	953	O	ALA	A	242	7.207	97.969	63.627	1.00	20.03	A	O

ATOM	954	N	LEU	A	243	6.050	96.088	63.195	1.00	21.54	A	N
ATOM	955	CA	LEU	A	243	6.111	96.281	61.742	1.00	23.33	A	C
ATOM	956	CB	LEU	A	243	5.617	95.029	61.014	1.00	21.31	A	C
ATOM	957	CG	LEU	A	243	6.556	93.828	61.128	1.00	21.88	A	C
ATOM	958	CD1	LEU	A	243	5.843	92.565	60.657	1.00	20.10	A	C
ATOM	959	CD2	LEU	A	243	7.802	94.085	60.305	1.00	18.75	A	C
ATOM	960	C	LEU	A	243	5.284	97.489	61.306	1.00	23.69	A	C
ATOM	961	O	LEU	A	243	5.627	98.171	60.344	1.00	22.16	A	O
ATOM	962	N	SER	A	244	4.191	97.741	62.021	1.00	25.47	A	N
ATOM	963	CA	SER	A	244	3.315	98.872	61.724	1.00	27.54	A	C
ATOM	964	CB	SER	A	244	2.053	98.784	62.584	1.00	28.75	A	C
ATOM	965	OG	SER	A	244	1.177	99.856	62.312	1.00	33.33	A	O
ATOM	966	C	SER	A	244	4.053	100.190	61.992	1.00	27.13	A	C
ATOM	967	O	SER	A	244	3.987	101.131	61.197	1.00	25.34	A	O
ATOM	968	N	TYR	A	245	4.757	100.253	63.117	1.00	27.39	A	N
ATOM	969	CA	TYR	A	245	5.518	101.444	63.455	1.00	26.91	A	C
ATOM	970	CB	TYR	A	245	6.122	101.303	64.862	1.00	26.66	A	C
ATOM	971	CG	TYR	A	245	7.181	102.328	65.192	1.00	26.43	A	C
ATOM	972	CD1	TYR	A	245	8.530	102.058	64.966	1.00	26.18	A	C
ATOM	973	CE1	TYR	A	245	9.517	103.008	65.248	1.00	27.41	A	C
ATOM	974	CD2	TYR	A	245	6.836	103.580	65.709	1.00	28.15	A	C
ATOM	975	CE2	TYR	A	245	7.815	104.539	65.994	1.00	27.61	A	C
ATOM	976	CZ	TYR	A	245	9.153	104.243	65.762	1.00	28.05	A	C
ATOM	977	OH	TYR	A	245	10.130	105.171	66.056	1.00	29.74	A	O
ATOM	978	C	TYR	A	245	6.612	101.653	62.402	1.00	26.52	A	C
ATOM	979	O	TYR	A	245	6.864	102.780	61.975	1.00	28.22	A	O
ATOM	980	N	CYS	A	246	7.254	100.573	61.970	1.00	26.10	A	N
ATOM	981	CA	CYS	A	246	8.305	100.683	60.957	1.00	27.26	A	C
ATOM	982	CB	CYS	A	246	8.973	99.320	60.703	1.00	25.76	A	C
ATOM	983	SG	CYS	A	246	10.111	98.729	62.011	1.00	25.61	A	S
ATOM	984	C	CYS	A	246	7.766	101.234	59.630	1.00	28.04	A	C
ATOM	985	O	CYS	A	246	8.357	102.139	59.041	1.00	28.18	A	O
ATOM	986	N	HIS	A	247	6.649	100.685	59.159	1.00	28.72	A	N
ATOM	987	CA	HIS	A	247	6.063	101.135	57.900	1.00	28.83	A	C
ATOM	988	CB	HIS	A	247	4.807	100.321	57.565	1.00	27.01	A	C
ATOM	989	CG	HIS	A	247	5.100	98.935	57.074	1.00	28.45	A	C
ATOM	990	CD2	HIS	A	247	6.274	98.296	56.851	1.00	29.49	A	C
ATOM	991	ND1	HIS	A	247	4.108	98.032	56.751	1.00	28.49	A	N
ATOM	992	CE1	HIS	A	247	4.658	96.898	56.354	1.00	27.81	A	C
ATOM	993	NE2	HIS	A	247	5.971	97.032	56.404	1.00	27.61	A	N
ATOM	994	C	HIS	A	247	5.757	102.627	57.921	1.00	28.03	A	C
ATOM	995	O	HIS	A	247	5.962	103.312	56.926	1.00	27.03	A	O
ATOM	996	N	SER	A	248	5.289	103.135	59.055	1.00	29.96	A	N
ATOM	997	CA	SER	A	248	4.996	104.568	59.172	1.00	31.71	A	C
ATOM	998	CB	SER	A	248	4.209	104.862	60.460	1.00	31.45	A	C
ATOM	999	OG	SER	A	248	4.988	104.617	61.622	1.00	32.11	A	O
ATOM	1000	C	SER	A	248	6.296	105.381	59.167	1.00	32.32	A	C
ATOM	1001	O	SER	A	248	6.276	106.604	59.039	1.00	33.26	A	O
ATOM	1002	N	LYS	A	249	7.426	104.694	59.310	1.00	33.45	A	N
ATOM	1003	CA	LYS	A	249	8.727	105.351	59.312	1.00	34.06	A	C
ATOM	1004	CB	LYS	A	249	9.572	104.883	60.506	1.00	35.23	A	C
ATOM	1005	CG	LYS	A	249	9.108	105.420	61.849	1.00	36.16	A	C
ATOM	1006	CD	LYS	A	249	9.142	106.947	61.870	1.00	38.50	A	C
ATOM	1007	CE	LYS	A	249	8.754	107.506	63.231	1.00	39.69	A	C
ATOM	1008	NZ	LYS	A	249	7.384	107.080	63.656	1.00	42.72	A	N
ATOM	1009	C	LYS	A	249	9.457	105.048	58.012	1.00	34.43	A	C
ATOM	1010	O	LYS	A	249	10.640	105.364	57.861	1.00	32.18	A	O
ATOM	1011	N	ARG	A	250	8.738	104.430	57.078	1.00	35.69	A	N
ATOM	1012	CA	ARG	A	250	9.288	104.081	55.778	1.00	37.56	A	C
ATOM	1013	CB	ARG	A	250	9.696	105.359	55.038	1.00	39.76	A	C
ATOM	1014	CG	ARG	A	250	8.501	106.132	54.453	1.00	41.59	A	C
ATOM	1015	CD	ARG	A	250	8.894	107.524	53.945	1.00	45.10	A	C
ATOM	1016	NE	ARG	A	250	8.232	107.855	52.679	1.00	47.20	A	N
ATOM	1017	CZ	ARG	A	250	8.713	107.536	51.478	1.00	47.18	A	C
ATOM	1018	NH1	ARG	A	250	9.865	106.884	51.374	1.00	46.33	A	N
ATOM	1019	NH2	ARG	A	250	8.042	107.863	50.381	1.00	45.77	A	N
ATOM	1020	C	ARG	A	250	10.465	103.118	55.890	1.00	39.53	A	C
ATOM	1021	O	ARG	A	250	11.451	103.225	55.162	1.00	38.88	A	O
ATOM	1022	N	VAL	A	251	10.348	102.169	56.813	1.00	41.36	A	N
ATOM	1023	CA	VAL	A	251	11.384	101.171	57.031	1.00	43.61	A	C
ATOM	1024	CB	VAL	A	251	11.846	101.171	58.500	1.00	43.34	A	C
ATOM	1025	CG1	VAL	A	251	12.834	100.031	58.745	1.00	42.55	A	C

ATOM	1026	CG2	VAL	A	251	12.479	102.512	58.834	1.00	41.90	A	C
ATOM	1027	C	VAL	A	251	10.864	99.782	56.672	1.00	45.77	A	C
ATOM	1028	O	VAL	A	251	9.773	99.393	57.087	1.00	45.19	A	O
ATOM	1029	N	ILE	A	252	11.013	98.979	55.608	1.00	48.92	A	N
ATOM	1030	CA	ILE	A	252	10.490	97.678	55.184	1.00	51.87	A	C
ATOM	1031	CB	ILE	A	252	10.035	97.701	53.702	1.00	51.65	A	C
ATOM	1032	CG2	ILE	A	252	9.532	96.322	53.292	1.00	52.57	A	C
ATOM	1033	CG1	ILE	A	252	8.929	98.741	53.511	1.00	50.23	A	C
ATOM	1034	CD1	ILE	A	252	9.375	100.169	53.722	1.00	48.71	A	C
ATOM	1035	C	ILE	A	252	11.630	96.682	55.358	1.00	53.81	A	C
ATOM	1036	O	ILE	A	252	12.743	96.924	54.895	1.00	53.23	A	O
ATOM	1037	N	HIS	A	253	11.359	95.564	56.019	1.00	57.15	A	N
ATOM	1038	CA	HIS	A	253	12.415	94.593	56.281	1.00	60.73	A	C
ATOM	1039	CB	HIS	A	253	12.150	93.878	57.606	1.00	61.57	A	C
ATOM	1040	CG	HIS	A	253	12.383	94.743	58.805	1.00	63.18	A	C
ATOM	1041	CD2	HIS	A	253	11.736	94.819	59.992	1.00	62.71	A	C
ATOM	1042	ND1	HIS	A	253	13.419	95.651	58.873	1.00	63.35	A	N
ATOM	1043	CE1	HIS	A	253	13.400	96.248	60.051	1.00	63.74	A	C
ATOM	1044	NE2	HIS	A	253	12.389	95.762	60.749	1.00	63.77	A	N
ATOM	1045	C	HIS	A	253	12.749	93.565	55.217	1.00	62.30	A	C
ATOM	1046	O	HIS	A	253	13.885	93.514	54.744	1.00	61.97	A	O
ATOM	1047	N	ARG	A	254	11.774	92.742	54.849	1.00	64.77	A	N
ATOM	1048	CA	ARG	A	254	12.004	91.700	53.855	1.00	66.63	A	C
ATOM	1049	CB	ARG	A	254	12.719	92.304	52.639	1.00	67.76	A	C
ATOM	1050	CG	ARG	A	254	11.948	93.473	52.021	1.00	69.83	A	C
ATOM	1051	CD	ARG	A	254	12.846	94.466	51.288	1.00	71.13	A	C
ATOM	1052	NE	ARG	A	254	13.615	93.863	50.203	1.00	71.83	A	N
ATOM	1053	CZ	ARG	A	254	14.438	94.543	49.410	1.00	72.27	A	C
ATOM	1054	NH1	ARG	A	254	14.596	95.850	49.580	1.00	72.84	A	N
ATOM	1055	NH2	ARG	A	254	15.107	93.917	48.450	1.00	72.64	A	N
ATOM	1056	C	ARG	A	254	12.858	90.603	54.507	1.00	67.14	A	C
ATOM	1057	O	ARG	A	254	13.356	89.699	53.830	1.00	67.13	A	O
ATOM	1058	N	ASP	A	255	13.002	90.694	55.832	1.00	67.58	A	N
ATOM	1059	CA	ASP	A	255	13.789	89.744	56.630	1.00	66.56	A	C
ATOM	1060	CB	ASP	A	255	15.286	90.046	56.458	1.00	67.69	A	C
ATOM	1061	CG	ASP	A	255	16.113	89.642	57.669	1.00	68.95	A	C
ATOM	1062	OD1	ASP	A	255	16.108	88.448	58.041	1.00	69.89	A	O
ATOM	1063	OD2	ASP	A	255	16.772	90.529	58.249	1.00	69.16	A	O
ATOM	1064	C	ASP	A	255	13.413	89.809	58.122	1.00	64.41	A	C
ATOM	1065	O	ASP	A	255	13.261	90.904	58.674	1.00	64.57	A	O
ATOM	1066	N	ILE	A	256	13.265	88.644	58.763	1.00	60.26	A	N
ATOM	1067	CA	ILE	A	256	12.918	88.587	60.186	1.00	56.43	A	C
ATOM	1068	CB	ILE	A	256	11.560	89.297	60.443	1.00	56.10	A	C
ATOM	1069	CG2	ILE	A	256	10.406	88.449	59.934	1.00	55.25	A	C
ATOM	1070	CG1	ILE	A	256	11.386	89.571	61.931	1.00	55.17	A	C
ATOM	1071	CD1	ILE	A	256	10.193	90.444	62.235	1.00	56.51	A	C
ATOM	1072	C	ILE	A	256	12.877	87.163	60.782	1.00	53.68	A	C
ATOM	1073	O	ILE	A	256	11.950	86.803	61.505	1.00	53.90	A	O
ATOM	1074	N	LYS	A	257	13.904	86.370	60.492	1.00	49.81	A	N
ATOM	1075	CA	LYS	A	257	14.008	84.992	60.975	1.00	46.01	A	C
ATOM	1076	CB	LYS	A	257	15.248	84.327	60.369	1.00	45.90	A	C
ATOM	1077	CG	LYS	A	257	15.162	84.086	58.880	1.00	48.40	A	C
ATOM	1078	CD	LYS	A	257	16.403	83.366	58.365	1.00	49.60	A	C
ATOM	1079	CE	LYS	A	257	17.628	84.250	58.442	1.00	49.74	A	C
ATOM	1080	NZ	LYS	A	257	17.476	85.429	57.544	1.00	51.45	A	N
ATOM	1081	C	LYS	A	257	14.070	84.838	62.498	1.00	42.23	A	C
ATOM	1082	O	LYS	A	257	14.379	85.783	63.218	1.00	42.43	A	O
ATOM	1083	N	PRO	A	258	13.822	84.410	63.074	1.00	38.37	A	N
ATOM	1084	CD	PRO	A	258	13.620	83.540	61.908	1.00	37.81	A	C
ATOM	1085	CA	PRO	A	258	13.838	83.621	64.315	1.00	36.58	A	C
ATOM	1086	CB	PRO	A	258	13.569	82.193	63.834	1.00	35.41	A	C
ATOM	1087	CG	PRO	A	258	12.869	82.383	62.514	1.00	35.75	A	C
ATOM	1088	C	PRO	A	258	15.216	83.756	64.962	1.00	35.92	A	C
ATOM	1089	O	PRO	A	258	15.333	84.057	66.151	1.00	32.14	A	O
ATOM	1090	N	GLU	A	259	16.249	83.523	64.155	1.00	35.08	A	N
ATOM	1091	CA	GLU	A	259	17.626	83.652	64.601	1.00	36.22	A	C
ATOM	1092	CB	GLU	A	259	18.607	83.198	63.506	1.00	37.23	A	C
ATOM	1093	CG	GLU	A	259	18.795	81.688	63.340	1.00	40.19	A	C
ATOM	1094	CD	GLU	A	259	17.713	81.010	62.496	1.00	42.23	A	C
ATOM	1095	OE1	GLU	A	259	17.915	79.827	62.142	1.00	41.52	A	O
ATOM	1096	OE2	GLU	A	259	16.670	81.642	62.192	1.00	40.30	A	O
ATOM	1097	C	GLU	A	259	17.863	85.132	64.870	1.00	35.71	A	C

ATOM	1098	O	GLU	A	259	18.700	85.499	65.688	1.00	35.67	A	O
ATOM	1099	N	ASN	A	260	17.114	85.980	64.171	1.00	35.37	A	N
ATOM	1100	CA	ASN	A	260	17.264	87.423	64.308	1.00	33.13	A	C
ATOM	1101	CB	ASN	A	260	17.209	88.081	62.927	1.00	34.73	A	C
ATOM	1102	CG	ASN	A	260	18.037	87.335	61.893	1.00	35.58	A	C
ATOM	1103	OD1	ASN	A	260	19.087	86.773	62.205	1.00	37.11	A	O
ATOM	1104	ND2	ASN	A	260	17.573	87.340	60.653	1.00	37.65	A	N
ATOM	1105	C	ASN	A	260	16.236	88.073	65.229	1.00	31.26	A	C
ATOM	1106	O	ASN	A	260	16.106	89.300	65.261	1.00	34.44	A	O
ATOM	1107	N	LEU	A	261	15.494	87.255	65.963	1.00	27.11	A	N
ATOM	1108	CA	LEU	A	261	14.501	87.762	66.902	1.00	24.52	A	C
ATOM	1109	CB	LEU	A	261	13.147	87.089	66.648	1.00	24.18	A	C
ATOM	1110	CG	LEU	A	261	12.432	87.443	65.340	1.00	22.90	A	C
ATOM	1111	CD1	LEU	A	261	11.116	86.685	65.252	1.00	24.50	A	C
ATOM	1112	CD2	LEU	A	261	12.172	88.923	65.296	1.00	21.37	A	C
ATOM	1113	C	LEU	A	261	14.986	87.476	68.329	1.00	22.38	A	C
ATOM	1114	O	LEU	A	261	15.179	86.321	68.694	1.00	23.95	A	O
ATOM	1115	N	LEU	A	262	15.182	88.524	69.126	1.00	20.79	A	N
ATOM	1116	CA	LEU	A	262	15.670	88.370	70.499	1.00	20.67	A	C
ATOM	1117	CB	LEU	A	262	16.810	89.376	70.758	1.00	18.51	A	C
ATOM	1118	CG	LEU	A	262	17.955	89.381	69.723	1.00	21.77	A	C
ATOM	1119	CD1	LEU	A	262	18.955	90.499	70.035	1.00	21.55	A	C
ATOM	1120	CD2	LEU	A	262	18.672	88.033	69.723	1.00	20.67	A	C
ATOM	1121	C	LEU	A	262	14.556	88.538	71.543	1.00	20.45	A	C
ATOM	1122	O	LEU	A	262	13.484	89.054	71.232	1.00	21.30	A	O
ATOM	1123	N	LEU	A	263	14.820	88.095	72.775	1.00	19.96	A	N
ATOM	1124	CA	LEU	A	263	13.855	88.172	73.875	1.00	20.52	A	C
ATOM	1125	CB	LEU	A	263	13.556	86.769	74.407	1.00	20.43	A	C
ATOM	1126	CG	LEU	A	263	12.804	85.816	73.471	1.00	22.66	A	C
ATOM	1127	CD1	LEU	A	263	12.979	84.366	73.956	1.00	21.47	A	C
ATOM	1128	CD2	LEU	A	263	11.330	86.219	73.415	1.00	19.52	A	C
ATOM	1129	C	LEU	A	263	14.307	89.045	75.046	1.00	22.38	A	C
ATOM	1130	O	LEU	A	263	15.389	88.848	75.603	1.00	22.70	A	O
ATOM	1131	N	GLY	A	264	13.456	89.992	75.429	1.00	21.30	A	N
ATOM	1132	CA	GLY	A	264	13.765	90.882	76.530	1.00	23.34	A	C
ATOM	1133	C	GLY	A	264	13.574	90.251	77.902	1.00	25.78	A	C
ATOM	1134	O	GLY	A	264	13.277	89.061	78.025	1.00	24.77	A	O
ATOM	1135	N	SER	A	265	13.732	91.067	78.939	1.00	27.28	A	N
ATOM	1136	CA	SER	A	265	13.618	90.609	80.321	1.00	28.82	A	C
ATOM	1137	CB	SER	A	265	13.959	91.758	81.270	1.00	29.98	A	C
ATOM	1138	OG	SER	A	265	14.174	91.285	82.583	1.00	31.27	A	O
ATOM	1139	C	SER	A	265	12.253	90.039	80.684	1.00	29.23	A	C
ATOM	1140	O	SER	A	265	12.158	89.086	81.449	1.00	30.53	A	O
ATOM	1141	N	ALA	A	266	11.193	90.623	80.140	1.00	29.57	A	N
ATOM	1142	CA	ALA	A	266	9.845	90.156	80.432	1.00	28.18	A	C
ATOM	1143	CB	ALA	A	266	8.889	91.338	80.475	1.00	28.62	A	C
ATOM	1144	C	ALA	A	266	9.378	89.141	79.399	1.00	27.11	A	C
ATOM	1145	O	ALA	A	266	8.211	88.749	79.393	1.00	29.47	A	O
ATOM	1146	N	GLY	A	267	10.274	88.717	78.524	1.00	25.83	A	N
ATOM	1147	CA	GLY	A	267	9.900	87.759	77.502	1.00	24.74	A	C
ATOM	1148	C	GLY	A	267	9.343	88.414	76.249	1.00	24.20	A	C
ATOM	1149	O	GLY	A	267	8.829	87.729	75.365	1.00	22.75	A	O
ATOM	1150	N	GLU	A	268	9.435	89.740	76.167	1.00	24.05	A	N
ATOM	1151	CA	GLU	A	268	8.942	90.468	74.993	1.00	25.88	A	C
ATOM	1152	CB	GLU	A	268	8.748	91.951	75.328	1.00	27.62	A	C
ATOM	1153	CG	GLU	A	268	8.880	92.266	76.803	1.00	33.71	A	C
ATOM	1154	CD	GLU	A	268	10.323	92.434	77.243	1.00	35.40	A	C
ATOM	1155	OE1	GLU	A	268	10.874	93.537	77.049	1.00	36.57	A	O
ATOM	1156	OE2	GLU	A	268	10.909	91.465	77.773	1.00	36.25	A	O
ATOM	1157	C	GLU	A	268	9.920	90.327	73.820	1.00	24.17	A	C
ATOM	1158	O	GLU	A	268	11.138	90.213	74.021	1.00	23.37	A	O
ATOM	1159	N	LEU	A	269	9.380	90.317	72.603	1.00	22.43	A	N
ATOM	1160	CA	LEU	A	269	10.185	90.189	71.388	1.00	22.74	A	C
ATOM	1161	CB	LEU	A	269	9.291	89.793	70.204	1.00	27.41	A	C
ATOM	1162	CG	LEU	A	269	8.760	88.370	70.198	1.00	30.77	A	C
ATOM	1163	CD1	LEU	A	269	7.689	88.219	69.115	1.00	32.33	A	C
ATOM	1164	CD2	LEU	A	269	9.893	87.387	69.981	1.00	30.69	A	C
ATOM	1165	C	LEU	A	269	10.941	91.466	71.024	1.00	20.79	A	C
ATOM	1166	O	LEU	A	269	10.427	92.569	71.176	1.00	20.86	A	O
ATOM	1167	N	LYS	A	270	12.164	91.310	70.536	1.00	19.07	A	N
ATOM	1168	CA	LYS	A	270	12.968	92.453	70.123	1.00	19.86	A	C
ATOM	1169	CB	LYS	A	270	14.179	92.628	71.046	1.00	19.41	A	C

ATOM	1170	CG	LYS	A	270	13.839	92.907	72.512	1.00	21.56	A	C
ATOM	1171	CD	LYS	A	270	13.368	94.336	72.739	1.00	21.90	A	C
ATOM	1172	CE	LYS	A	270	13.083	94.578	74.222	1.00	19.95	A	C
ATOM	1173	NZ	LYS	A	270	12.812	96.006	74.509	1.00	19.75	A	N
ATOM	1174	C	LYS	A	270	13.459	92.201	68.703	1.00	19.52	A	C
ATOM	1175	O	LYS	A	270	14.126	91.199	68.458	1.00	19.94	A	O
ATOM	1176	N	ILE	A	271	13.122	93.092	67.768	1.00	20.30	A	N
ATOM	1177	CA	ILE	A	271	13.581	92.946	66.388	1.00	19.95	A	C
ATOM	1178	CB	ILE	A	271	12.637	93.645	65.375	1.00	21.57	A	C
ATOM	1179	CG2	ILE	A	271	13.245	93.602	63.959	1.00	22.31	A	C
ATOM	1180	CG1	ILE	A	271	11.275	92.952	65.349	1.00	23.31	A	C
ATOM	1181	CD1	ILE	A	271	10.313	93.557	64.325	1.00	23.77	A	C
ATOM	1182	C	ILE	A	271	14.966	93.584	66.273	1.00	20.17	A	C
ATOM	1183	O	ILE	A	271	15.139	94.761	66.590	1.00	19.60	A	O
ATOM	1184	N	ALA	A	272	15.945	92.805	65.822	1.00	20.80	A	N
ATOM	1185	CA	ALA	A	272	17.318	93.291	65.675	1.00	22.55	A	C
ATOM	1186	CB	ALA	A	272	18.278	92.307	66.319	1.00	22.63	A	C
ATOM	1187	C	ALA	A	272	17.671	93.477	64.199	1.00	23.77	A	C
ATOM	1188	O	ALA	A	272	16.967	92.985	63.335	1.00	27.69	A	O
ATOM	1189	N	ASP	A	273	18.770	94.166	63.914	1.00	25.21	A	N
ATOM	1190	CA	ASP	A	273	19.179	94.423	62.535	1.00	26.15	A	C
ATOM	1191	CB	ASP	A	273	19.470	95.919	62.371	1.00	26.59	A	C
ATOM	1192	CG	ASP	A	273	19.481	96.364	60.922	1.00	28.71	A	C
ATOM	1193	OD1	ASP	A	273	19.921	97.503	60.662	1.00	27.94	A	O
ATOM	1194	OD2	ASP	A	273	19.042	95.587	60.048	1.00	26.80	A	O
ATOM	1195	C	ASP	A	273	20.409	93.608	62.114	1.00	28.69	A	C
ATOM	1196	O	ASP	A	273	21.513	94.134	62.036	1.00	31.16	A	O
ATOM	1197	N	PHE	A	274	20.212	92.325	61.825	1.00	31.46	A	N
ATOM	1198	CA	PHE	A	274	21.309	91.445	61.410	1.00	34.17	A	C
ATOM	1199	CB	PHE	A	274	21.014	90.005	61.826	1.00	34.86	A	C
ATOM	1200	CG	PHE	A	274	21.126	89.762	63.298	1.00	34.01	A	C
ATOM	1201	CD1	PHE	A	274	22.369	89.593	63.891	1.00	35.57	A	C
ATOM	1202	CD2	PHE	A	274	19.986	89.690	64.091	1.00	33.84	A	C
ATOM	1203	CE1	PHE	A	274	22.478	89.352	65.255	1.00	34.13	A	C
ATOM	1204	CE2	PHE	A	274	20.075	89.449	65.458	1.00	33.04	A	C
ATOM	1205	CZ	PHE	A	274	21.315	89.279	66.043	1.00	35.67	A	C
ATOM	1206	C	PHE	A	274	21.610	91.465	59.908	1.00	35.98	A	C
ATOM	1207	O	PHE	A	274	22.769	91.357	59.508	1.00	37.36	A	O
ATOM	1208	N	GLY	A	275	20.591	91.607	59.065	1.00	36.77	A	N
ATOM	1209	CA	GLY	A	275	20.879	91.613	57.640	1.00	38.21	A	C
ATOM	1210	C	GLY	A	275	21.125	93.012	57.108	1.00	39.96	A	C
ATOM	1211	O	GLY	A	275	20.645	93.371	56.030	1.00	40.54	A	O
ATOM	1212	N	TRP	A	276	21.894	93.801	57.850	1.00	40.99	A	N
ATOM	1213	CA	TRP	A	276	22.180	95.178	57.454	1.00	41.46	A	C
ATOM	1214	CB	TRP	A	276	22.767	95.958	58.633	1.00	39.82	A	C
ATOM	1215	CG	TRP	A	276	24.099	95.435	59.065	1.00	39.01	A	C
ATOM	1216	CD2	TRP	A	276	25.379	95.801	58.523	1.00	38.81	A	C
ATOM	1217	CE2	TRP	A	276	26.350	95.024	59.190	1.00	38.69	A	C
ATOM	1218	CE3	TRP	A	276	25.790	96.707	57.538	1.00	38.86	A	C
ATOM	1219	CD1	TRP	A	276	24.344	94.481	60.014	1.00	37.17	A	C
ATOM	1220	NE1	TRP	A	276	25.692	94.231	60.092	1.00	36.72	A	N
ATOM	1221	CZ2	TRP	A	276	27.717	95.125	58.905	1.00	39.22	A	C
ATOM	1222	CZ3	TRP	A	276	27.154	96.809	57.249	1.00	40.49	A	C
ATOM	1223	CH2	TRP	A	276	28.101	96.018	57.934	1.00	39.41	A	C
ATOM	1224	C	TRP	A	276	23.152	95.244	56.289	1.00	42.15	A	C
ATOM	1225	O	TRP	A	276	23.334	96.307	55.686	1.00	43.44	A	O
ATOM	1226	N	SER	A	277	23.790	94.119	55.982	1.00	42.35	A	N
ATOM	1227	CA	SER	A	277	24.750	94.058	54.887	1.00	43.23	A	C
ATOM	1228	CB	SER	A	277	26.063	93.415	55.360	1.00	42.06	A	C
ATOM	1229	OG	SER	A	277	25.810	92.188	56.032	1.00	41.30	A	O
ATOM	1230	C	SER	A	277	24.171	93.244	53.736	1.00	44.99	A	C
ATOM	1231	O	SER	A	277	24.709	93.259	52.619	1.00	46.90	A	O
ATOM	1232	N	GLY	A	290	19.559	85.906	54.593	1.00	50.58	A	N
ATOM	1233	CA	GLY	A	290	18.167	85.530	54.418	1.00	50.41	A	C
ATOM	1234	C	GLY	A	290	17.976	84.405	53.413	1.00	49.78	A	C
ATOM	1235	O	GLY	A	290	17.787	84.652	52.215	1.00	49.58	A	O
ATOM	1236	N	THR	A	291	18.024	83.166	53.899	1.00	47.99	A	N
ATOM	1237	CA	THR	A	291	17.855	82.001	53.036	1.00	45.67	A	C
ATOM	1238	CB	THR	A	291	17.993	80.671	53.833	1.00	46.93	A	C
ATOM	1239	OG1	THR	A	291	17.389	80.818	55.127	1.00	47.18	A	O
ATOM	1240	CG2	THR	A	291	19.460	80.279	53.988	1.00	45.73	A	C
ATOM	1241	C	THR	A	291	16.504	82.009	52.318	1.00	43.16	A	C

ATOM	1242	O	THR	A	291	15.604	82.783	52.650	1.00	42.03	A	O
ATOM	1243	N	LEU	A	292	16.385	81.119	51.340	1.00	41.25	A	N
ATOM	1244	CA	LEU	A	292	15.194	80.972	50.514	1.00	39.15	A	C
ATOM	1245	CB	LEU	A	292	15.417	79.814	49.540	1.00	41.13	A	C
ATOM	1246	CG	LEU	A	292	14.653	79.815	48.220	1.00	41.33	A	C
ATOM	1247	CD1	LEU	A	292	14.961	81.085	47.436	1.00	40.19	A	C
ATOM	1248	CD2	LEU	A	292	15.069	78.592	47.423	1.00	43.53	A	C
ATOM	1249	C	LEU	A	292	13.887	80.750	51.280	1.00	36.22	A	C
ATOM	1250	O	LEU	A	292	12.847	81.287	50.909	1.00	35.72	A	O
ATOM	1251	N	ASP	A	293	13.949	79.964	52.346	1.00	32.89	A	N
ATOM	1252	CA	ASP	A	293	12.771	79.647	53.150	1.00	31.62	A	C
ATOM	1253	CB	ASP	A	293	13.211	78.945	54.437	1.00	31.49	A	C
ATOM	1254	CG	ASP	A	293	13.399	77.452	54.253	1.00	33.23	A	C
ATOM	1255	OD1	ASP	A	293	14.114	76.838	55.076	1.00	35.49	A	O
ATOM	1256	OD2	ASP	A	293	12.818	76.886	53.299	1.00	31.43	A	O
ATOM	1257	C	ASP	A	293	11.805	80.779	53.503	1.00	29.72	A	C
ATOM	1258	O	ASP	A	293	10.595	80.563	53.556	1.00	28.20	A	O
ATOM	1259	N	TYR	A	294	12.327	81.977	53.748	1.00	28.61	A	N
ATOM	1260	CA	TYR	A	294	11.476	83.101	54.128	1.00	27.28	A	C
ATOM	1261	CB	TYR	A	294	12.064	83.814	55.357	1.00	28.14	A	C
ATOM	1262	CG	TYR	A	294	12.451	82.871	56.472	1.00	29.60	A	C
ATOM	1263	CD1	TYR	A	294	13.669	82.192	56.442	1.00	31.65	A	C
ATOM	1264	CE1	TYR	A	294	14.003	81.264	57.423	1.00	33.54	A	C
ATOM	1265	CD2	TYR	A	294	11.574	82.601	57.522	1.00	31.90	A	C
ATOM	1266	CE2	TYR	A	294	11.897	81.669	58.514	1.00	32.48	A	C
ATOM	1267	CZ	TYR	A	294	13.112	81.005	58.454	1.00	35.17	A	C
ATOM	1268	OH	TYR	A	294	13.437	80.065	59.406	1.00	37.45	A	O
ATOM	1269	C	TYR	A	294	11.211	84.126	53.032	1.00	26.29	A	C
ATOM	1270	O	TYR	A	294	10.530	85.117	53.276	1.00	27.19	A	O
ATOM	1271	N	LEU	A	295	11.732	83.888	51.830	1.00	25.16	A	N
ATOM	1272	CA	LEU	A	295	11.540	84.809	50.709	1.00	24.82	A	C
ATOM	1273	CB	LEU	A	295	12.643	84.607	49.669	1.00	24.50	A	C
ATOM	1274	CG	LEU	A	295	14.052	85.044	50.075	1.00	25.62	A	C
ATOM	1275	CD1	LEU	A	295	15.019	84.731	48.952	1.00	21.99	A	C
ATOM	1276	CD2	LEU	A	295	14.053	86.535	50.391	1.00	25.81	A	C
ATOM	1277	C	LEU	A	295	10.181	84.671	50.019	1.00	22.65	A	C
ATOM	1278	O	LEU	A	295	9.736	83.565	49.730	1.00	22.45	A	O
ATOM	1279	N	PRO	A	296	9.515	85.800	49.730	1.00	21.47	A	N
ATOM	1280	CD	PRO	A	296	9.864	87.159	50.187	1.00	22.06	A	C
ATOM	1281	CA	PRO	A	296	8.202	85.782	49.066	1.00	21.33	A	C
ATOM	1282	CB	PRO	A	296	7.634	87.169	49.380	1.00	20.33	A	C
ATOM	1283	CG	PRO	A	296	8.888	88.033	49.450	1.00	21.76	A	C
ATOM	1284	C	PRO	A	296	8.260	85.479	47.561	1.00	22.16	A	C
ATOM	1285	O	PRO	A	296	9.292	85.652	46.917	1.00	19.11	A	O
ATOM	1286	N	PRO	A	297	7.137	85.032	46.976	1.00	23.42	A	N
ATOM	1287	CD	PRO	A	297	5.799	84.826	47.557	1.00	21.93	A	C
ATOM	1288	CA	PRO	A	297	7.141	84.720	45.542	1.00	24.58	A	C
ATOM	1289	CB	PRO	A	297	5.693	84.315	45.271	1.00	24.85	A	C
ATOM	1290	CG	PRO	A	297	5.220	83.791	46.629	1.00	22.35	A	C
ATOM	1291	C	PRO	A	297	7.602	85.869	44.641	1.00	26.51	A	C
ATOM	1292	O	PRO	A	297	8.425	85.667	43.749	1.00	24.25	A	O
ATOM	1293	N	GLU	A	298	7.081	87.070	44.884	1.00	28.74	A	N
ATOM	1294	CA	GLU	A	298	7.435	88.231	44.070	1.00	32.43	A	C
ATOM	1295	CB	GLU	A	298	6.792	89.508	44.625	1.00	31.92	A	C
ATOM	1296	CG	GLU	A	298	7.073	89.780	46.093	1.00	31.41	A	C
ATOM	1297	CD	GLU	A	298	5.970	89.259	46.993	1.00	31.60	A	C
ATOM	1298	OE1	GLU	A	298	5.566	88.089	46.835	1.00	32.77	A	O
ATOM	1299	OE2	GLU	A	298	5.504	90.017	47.864	1.00	32.41	A	O
ATOM	1300	C	GLU	A	298	8.937	88.440	43.934	1.00	34.76	A	C
ATOM	1301	O	GLU	A	298	9.400	88.836	42.872	1.00	34.79	A	O
ATOM	1302	N	MET	A	299	9.679	88.167	45.003	1.00	37.58	A	N
ATOM	1303	CA	MET	A	299	11.121	88.348	44.966	1.00	39.94	A	C
ATOM	1304	CB	MET	A	299	11.676	88.481	46.391	1.00	40.17	A	C
ATOM	1305	CG	MET	A	299	11.251	89.800	47.055	1.00	40.44	A	C
ATOM	1306	SD	MET	A	299	11.866	90.123	48.737	1.00	42.44	A	S
ATOM	1307	CE	MET	A	299	13.408	90.986	48.365	1.00	41.54	A	C
ATOM	1308	C	MET	A	299	11.857	87.268	44.179	1.00	41.00	A	C
ATOM	1309	O	MET	A	299	12.582	87.589	43.237	1.00	42.71	A	O
ATOM	1310	N	ILE	A	300	11.674	85.998	44.525	1.00	42.03	A	N
ATOM	1311	CA	ILE	A	300	12.363	84.941	43.784	1.00	43.81	A	C
ATOM	1312	CB	ILE	A	300	12.140	83.535	44.407	1.00	44.39	A	C
ATOM	1313	CG2	ILE	A	300	12.690	83.497	45.829	1.00	45.06	A	C

	ATOM	1314	CG1	ILE	A	300	10.656	83.172	44.378	1.00	44.10	A C
	ATOM	1315	CD1	ILE	A	300	10.379	81.745	44.804	1.00	44.41	A C
	ATOM	1316	C	ILE	A	300	11.906	84.908	42.323	1.00	44.98	A C
	ATOM	1317	O	ILE	A	300	12.573	84.322	41.472	1.00	45.46	A O
5	ATOM	1318	N	GLU	A	301	10.762	85.529	42.042	1.00	45.85	A N
	ATOM	1319	CA	GLU	A	301	10.232	85.592	40.682	1.00	46.66	A C
	ATOM	1320	CB	GLU	A	301	8.709	85.477	40.687	1.00	47.45	A C
	ATOM	1321	CG	GLU	A	301	8.189	84.054	40.721	1.00	48.05	A C
	ATOM	1322	CD	GLU	A	301	6.688	83.997	40.916	1.00	49.14	A C
10	ATOM	1323	OE1	GLU	A	301	5.979	84.782	40.253	1.00	50.01	A O
	ATOM	1324	OE2	GLU	A	301	6.218	83.166	41.724	1.00	48.90	A O
	ATOM	1325	C	GLU	A	301	10.643	86.904	40.026	1.00	47.81	A C
	ATOM	1326	O	GLU	A	301	10.048	87.326	39.035	1.00	47.15	A O
	ATOM	1327	N	GLY	A	302	11.650	87.547	40.613	1.00	49.04	A N
15	ATOM	1328	CA	GLY	A	302	12.193	88.792	40.094	1.00	50.61	A C
	ATOM	1329	C	GLY	A	302	11.296	89.991	39.844	1.00	51.92	A C
	ATOM	1330	O	GLY	A	302	11.642	90.841	39.025	1.00	52.54	A O
	ATOM	1331	N	ARG	A	303	10.167	90.087	40.542	1.00	52.91	A N
	ATOM	1332	CA	ARG	A	303	9.259	91.219	40.356	1.00	53.57	A C
20	ATOM	1333	CB	ARG	A	303	7.812	90.753	40.529	1.00	55.04	A C
	ATOM	1334	CG	ARG	A	303	7.494	89.500	39.724	1.00	58.17	A C
	ATOM	1335	CD	ARG	A	303	6.011	89.149	39.750	1.00	60.28	A C
	ATOM	1336	NE	ARG	A	303	5.212	90.072	38.947	1.00	62.73	A N
	ATOM	1337	CZ	ARG	A	303	3.919	89.903	38.680	1.00	63.00	A C
25	ATOM	1338	NH1	ARG	A	303	3.271	90.794	37.941	1.00	62.86	A N
	ATOM	1339	NH2	ARG	A	303	3.275	88.842	39.150	1.00	62.02	A N
	ATOM	1340	C	ARG	A	303	9.571	92.371	41.320	1.00	52.69	A C
	ATOM	1341	O	ARG	A	303	10.582	92.344	42.020	1.00	52.06	A O
	ATOM	1342	N	MET	A	304	8.710	93.385	41.344	1.00	52.57	A N
30	ATOM	1343	CA	MET	A	304	8.907	94.539	42.223	1.00	52.97	A C
	ATOM	1344	CB	MET	A	304	8.395	95.820	41.542	1.00	55.47	A C
	ATOM	1345	CG	MET	A	304	8.972	97.135	42.103	1.00	59.08	A C
	ATOM	1346	SD	MET	A	304	7.948	98.022	43.326	1.00	62.23	A S
	ATOM	1347	CE	MET	A	304	7.208	99.317	42.301	1.00	60.78	A C
35	ATOM	1348	C	MET	A	304	8.153	94.299	43.526	1.00	51.89	A C
	ATOM	1349	O	MET	A	304	7.026	93.809	43.511	1.00	51.02	A O
	ATOM	1350	N	HIS	A	305	8.775	94.645	44.651	1.00	50.91	A N
	ATOM	1351	CA	HIS	A	305	8.149	94.441	45.953	1.00	49.66	A C
	ATOM	1352	CB	HIS	A	305	8.944	93.415	46.762	1.00	51.52	A C
40	ATOM	1353	CG	HIS	A	305	10.392	93.763	46.926	1.00	54.62	A C
	ATOM	1354	CD2	HIS	A	305	11.085	94.211	48.000	1.00	54.89	A C
	ATOM	1355	ND1	HIS	A	305	11.304	93.665	45.897	1.00	55.05	A N
	ATOM	1356	CE1	HIS	A	305	12.496	94.034	46.330	1.00	55.54	A C
	ATOM	1357	NE2	HIS	A	305	12.391	94.371	47.603	1.00	55.94	A N
45	ATOM	1358	C	HIS	A	305	7.996	95.712	46.778	1.00	47.80	A C
	ATOM	1359	O	HIS	A	305	8.620	96.730	46.491	1.00	47.81	A O
	ATOM	1360	N	ASP	A	306	7.150	95.635	47.802	1.00	45.38	A N
	ATOM	1361	CA	ASP	A	306	6.903	96.746	48.713	1.00	43.84	A C
	ATOM	1362	CB	ASP	A	306	5.667	97.548	48.278	1.00	44.46	A C
50	ATOM	1363	CG	ASP	A	306	4.424	96.691	48.154	1.00	45.21	A C
	ATOM	1364	OD1	ASP	A	306	4.233	95.727	48.935	1.00	45.61	A O
	ATOM	1365	OD2	ASP	A	306	3.579	96.992	47.285	1.00	45.96	A O
	ATOM	1366	C	ASP	A	306	6.714	96.213	50.141	1.00	42.01	A C
	ATOM	1367	O	ASP	A	306	7.276	95.181	50.498	1.00	40.43	A O
55	ATOM	1368	N	GLU	A	307	5.917	96.910	50.948	1.00	41.41	A N
	ATOM	1369	CA	GLU	A	307	5.684	96.503	52.334	1.00	40.47	A C
	ATOM	1370	CB	GLU	A	307	5.047	97.658	53.116	1.00	43.34	A C
	ATOM	1371	CG	GLU	A	307	3.673	98.084	52.624	1.00	49.09	A C
	ATOM	1372	CD	GLU	A	307	2.543	97.317	53.287	1.00	53.33	A C
60	ATOM	1373	OE1	GLU	A	307	1.369	97.561	52.933	1.00	56.15	A O
	ATOM	1374	OE2	GLU	A	307	2.822	96.475	54.168	1.00	56.15	A O
	ATOM	1375	C	GLU	A	307	4.838	95.236	52.486	1.00	37.15	A C
	ATOM	1376	O	GLU	A	307	4.555	94.774	53.603	1.00	36.77	A O
	ATOM	1377	N	LYS	A	308	4.402	94.668	51.367	1.00	33.66	A N
65	ATOM	1378	CA	LYS	A	308	3.599	93.455	51.411	1.00	29.96	A C
	ATOM	1379	CB	LYS	A	308	2.842	93.262	50.095	1.00	31.75	A C
	ATOM	1380	CG	LYS	A	308	1.668	94.214	49.908	1.00	30.26	A C
	ATOM	1381	CD	LYS	A	308	0.631	94.005	50.994	1.00	30.93	A C
	ATOM	1382	CE	LYS	A	308	-0.590	94.881	50.766	1.00	33.18	A C
70	ATOM	1383	NZ	LYS	A	308	-1.687	94.574	51.722	1.00	31.42	A N
	ATOM	1384	C	LYS	A	308	4.452	92.227	51.704	1.00	28.16	A C
	ATOM	1385	O	LYS	A	308	3.918	91.178	52.055	1.00	26.90	A O

ATOM	1386	N	VAL	A	309	5.772	92.354	51.566	1.00	26.12	A	N
ATOM	1387	CA	VAL	A	309	6.666	91.230	51.849	1.00	27.15	A	C
ATOM	1388	CB	VAL	A	309	8.147	91.546	51.483	1.00	28.50	A	C
ATOM	1389	CG1	VAL	A	309	8.273	91.828	49.988	1.00	28.82	A	C
ATOM	1390	CG2	VAL	A	309	8.648	92.728	52.299	1.00	28.83	A	C
ATOM	1391	C	VAL	A	309	6.608	90.885	53.339	1.00	27.51	A	C
ATOM	1392	O	VAL	A	309	6.748	89.720	53.725	1.00	28.44	A	O
ATOM	1393	N	ASP	A	310	6.382	91.905	54.167	1.00	25.49	A	N
ATOM	1394	CA	ASP	A	310	6.308	91.715	55.607	1.00	23.57	A	C
ATOM	1395	CB	ASP	A	310	6.281	93.069	56.332	1.00	23.42	A	C
ATOM	1396	CG	ASP	A	310	7.564	93.858	56.139	1.00	26.52	A	C
ATOM	1397	OD1	ASP	A	310	8.657	93.249	56.164	1.00	26.12	A	O
ATOM	1398	OD2	ASP	A	310	7.489	95.095	55.974	1.00	28.59	A	O
ATOM	1399	C	ASP	A	310	5.106	90.878	56.012	1.00	21.40	A	C
ATOM	1400	O	ASP	A	310	5.147	90.193	57.038	1.00	21.03	A	O
ATOM	1401	N	LEU	A	311	4.032	90.932	55.228	1.00	20.72	A	N
ATOM	1402	CA	LEU	A	311	2.848	90.126	55.541	1.00	20.20	A	C
ATOM	1403	CB	LEU	A	311	1.628	90.564	54.713	1.00	19.65	A	C
ATOM	1404	CG	LEU	A	311	0.794	91.785	55.141	1.00	21.99	A	C
ATOM	1405	CD1	LEU	A	311	0.255	91.575	56.547	1.00	23.33	A	C
ATOM	1406	CD2	LEU	A	311	1.635	93.047	55.092	1.00	23.76	A	C
ATOM	1407	C	LEU	A	311	3.171	88.658	55.238	1.00	18.99	A	C
ATOM	1408	O	LEU	A	311	2.764	87.760	55.960	1.00	16.87	A	O
ATOM	1409	N	TRP	A	312	3.892	88.424	54.148	1.00	19.04	A	N
ATOM	1410	CA	TRP	A	312	4.284	87.069	53.786	1.00	19.16	A	C
ATOM	1411	CB	TRP	A	312	5.094	87.083	52.482	1.00	19.35	A	C
ATOM	1412	CG	TRP	A	312	5.628	85.742	52.102	1.00	18.58	A	C
ATOM	1413	CD2	TRP	A	312	4.970	84.762	51.294	1.00	17.19	A	C
ATOM	1414	CE2	TRP	A	312	5.813	83.629	51.242	1.00	16.50	A	C
ATOM	1415	CE3	TRP	A	312	3.747	84.730	50.607	1.00	17.90	A	C
ATOM	1416	CD1	TRP	A	312	6.815	85.184	52.496	1.00	19.08	A	C
ATOM	1417	NE1	TRP	A	312	6.933	83.911	51.983	1.00	18.08	A	N
ATOM	1418	CZ2	TRP	A	312	5.473	82.478	50.533	1.00	17.00	A	C
ATOM	1419	CZ3	TRP	A	312	3.409	83.580	49.899	1.00	14.87	A	C
ATOM	1420	CH2	TRP	A	312	4.271	82.470	49.870	1.00	19.28	A	C
ATOM	1421	C	TRP	A	312	5.142	86.497	54.923	1.00	18.64	A	C
ATOM	1422	O	TRP	A	312	4.883	85.396	55.424	1.00	16.66	A	O
ATOM	1423	N	SER	A	313	6.154	87.259	55.333	1.00	15.99	A	N
ATOM	1424	CA	SER	A	313	7.043	86.823	56.408	1.00	18.14	A	C
ATOM	1425	CB	SER	A	313	8.034	87.931	56.760	1.00	18.03	A	C
ATOM	1426	OG	SER	A	313	8.747	88.320	55.604	1.00	20.11	A	O
ATOM	1427	C	SER	A	313	6.254	86.450	57.650	1.00	15.82	A	C
ATOM	1428	O	SER	A	313	6.538	85.460	58.303	1.00	16.33	A	O
ATOM	1429	N	LEU	A	314	5.251	87.249	57.967	1.00	17.05	A	N
ATOM	1430	CA	LEU	A	314	4.429	86.997	59.137	1.00	18.31	A	C
ATOM	1431	CB	LEU	A	314	3.408	88.136	59.273	1.00	21.36	A	C
ATOM	1432	CG	LEU	A	314	3.115	88.707	60.664	1.00	25.08	A	C
ATOM	1433	CD1	LEU	A	314	4.403	89.035	61.393	1.00	26.53	A	C
ATOM	1434	CD2	LEU	A	314	2.258	89.954	60.524	1.00	26.95	A	C
ATOM	1435	C	LEU	A	314	3.736	85.627	59.044	1.00	17.43	A	C
ATOM	1436	O	LEU	A	314	3.565	84.928	60.046	1.00	16.65	A	O
ATOM	1437	N	GLY	A	315	3.348	85.242	57.835	1.00	17.42	A	N
ATOM	1438	CA	GLY	A	315	2.682	83.961	57.646	1.00	16.42	A	C
ATOM	1439	C	GLY	A	315	3.623	82.781	57.799	1.00	13.19	A	C
ATOM	1440	O	GLY	A	315	3.275	81.775	58.411	1.00	12.24	A	O
ATOM	1441	N	VAL	A	316	4.816	82.900	57.231	1.00	11.93	A	N
ATOM	1442	CA	VAL	A	316	5.810	81.844	57.322	1.00	12.52	A	C
ATOM	1443	CB	VAL	A	316	7.085	82.225	56.521	1.00	14.29	A	C
ATOM	1444	CG1	VAL	A	316	8.233	81.270	56.858	1.00	9.03	A	C
ATOM	1445	CG2	VAL	A	316	6.779	82.186	55.011	1.00	11.86	A	C
ATOM	1446	C	VAL	A	316	6.182	81.591	58.784	1.00	15.03	A	C
ATOM	1447	O	VAL	A	316	6.310	80.446	59.213	1.00	17.62	A	O
ATOM	1448	N	LEU	A	317	6.343	82.679	59.534	1.00	14.58	A	N
ATOM	1449	CA	LEU	A	317	6.709	82.651	60.945	1.00	16.47	A	C
ATOM	1450	CB	LEU	A	317	7.311	84.077	61.402	1.00	19.62	A	C
ATOM	1451	CG	LEU	A	317	8.077	84.260	62.478	1.00	23.94	A	C
ATOM	1452	CD1	LEU	A	317	9.386	83.649	61.992	1.00	23.88	A	C
ATOM	1453	CD2	LEU	A	317	8.256	85.742	62.782	1.00	25.46	A	C
ATOM	1454	C	LEU	A	317	5.618	82.058	61.837	1.00	17.53	A	C
ATOM	1455	O	LEU	A	317	5.897	81.270	62.752	1.00	16.69	A	O
ATOM	1456	N	CYS	A	318	4.371	82.444	61.578	1.00	15.98	A	N
ATOM	1457	CA	CYS	A	318	3.272	81.937	62.380	1.00	15.13	A	C

ATOM	1458	CB	CYS	A	318	1.940	82.520	61.898	1.00	13.25	A	C
ATOM	1459	SG	CYS	A	318	0.563	82.056	62.970	1.00	20.95	A	S
ATOM	1460	C	CYS	A	318	3.253	80.420	62.263	1.00	14.70	A	C
ATOM	1461	O	CYS	A	318	3.087	79.710	63.245	1.00	13.83	A	O
ATOM	1462	N	TYR	A	319	3.421	79.942	61.038	1.00	15.03	A	N
ATOM	1463	CA	TYR	A	319	3.444	78.518	60.742	1.00	15.40	A	C
ATOM	1464	CB	TYR	A	319	3.583	78.317	59.226	1.00	14.02	A	C
ATOM	1465	CG	TYR	A	319	3.545	76.875	58.766	1.00	14.42	A	C
ATOM	1466	CD1	TYR	A	319	4.651	76.036	58.902	1.00	13.77	A	C
ATOM	1467	CE1	TYR	A	319	4.612	74.713	58.446	1.00	16.09	A	C
ATOM	1468	CD2	TYR	A	319	2.396	76.357	58.167	1.00	17.16	A	C
ATOM	1469	CE2	TYR	A	319	2.345	75.047	57.710	1.00	15.61	A	C
ATOM	1470	CZ	TYR	A	319	3.445	74.231	57.849	1.00	16.40	A	C
ATOM	1471	OH	TYR	A	319	3.363	72.937	57.385	1.00	15.59	A	O
ATOM	1472	C	TYR	A	319	4.610	77.831	61.462	1.00	15.16	A	C
ATOM	1473	O	TYR	A	319	4.407	76.869	62.193	1.00	14.51	A	O
ATOM	1474	N	GLU	A	320	5.828	78.330	61.246	1.00	17.29	A	N
ATOM	1475	CA	GLU	A	320	7.000	77.734	61.880	1.00	17.27	A	C
ATOM	1476	CB	GLU	A	320	8.281	78.487	61.507	1.00	18.78	A	C
ATOM	1477	CG	GLU	A	320	9.537	77.819	62.068	1.00	22.31	A	C
ATOM	1478	CD	GLU	A	320	10.838	78.346	61.469	1.00	26.99	A	C
ATOM	1479	OE1	GLU	A	320	11.904	77.777	61.784	1.00	27.38	A	O
ATOM	1480	OE2	GLU	A	320	10.807	79.319	60.692	1.00	26.89	A	O
ATOM	1481	C	GLU	A	320	6.845	77.672	63.404	1.00	17.31	A	C
ATOM	1482	O	GLU	A	320	7.234	76.689	64.019	1.00	16.67	A	O
ATOM	1483	N	PHE	A	321	6.259	78.702	64.006	1.00	17.96	A	N
ATOM	1484	CA	PHE	A	321	6.057	78.697	65.458	1.00	18.82	A	C
ATOM	1485	CB	PHE	A	321	5.387	79.993	65.948	1.00	18.10	A	C
ATOM	1486	CG	PHE	A	321	6.318	81.180	66.061	1.00	20.78	A	C
ATOM	1487	CD1	PHE	A	321	7.705	81.017	66.064	1.00	21.45	A	C
ATOM	1488	CD2	PHE	A	321	5.796	82.472	66.152	1.00	20.42	A	C
ATOM	1489	CE1	PHE	A	321	8.554	82.127	66.150	1.00	21.67	A	C
ATOM	1490	CE2	PHE	A	321	6.632	83.587	66.238	1.00	21.82	A	C
ATOM	1491	CZ	PHE	A	321	8.013	83.417	66.236	1.00	21.08	A	C
ATOM	1492	C	PHE	A	321	5.174	77.530	65.896	1.00	19.26	A	C
ATOM	1493	O	PHE	A	321	5.466	76.848	66.878	1.00	18.07	A	O
ATOM	1494	N	LEU	A	322	4.089	77.309	65.159	1.00	18.30	A	N
ATOM	1495	CA	LEU	A	322	3.134	76.258	65.498	1.00	18.16	A	C
ATOM	1496	CB	LEU	A	322	1.777	76.572	64.859	1.00	17.23	A	C
ATOM	1497	CG	LEU	A	322	1.016	77.755	65.455	1.00	16.28	A	C
ATOM	1498	CD1	LEU	A	322	-0.332	78.162	64.528	1.00	20.13	A	C
ATOM	1499	CD2	LEU	A	322	0.490	77.372	66.833	1.00	14.25	A	C
ATOM	1500	C	LEU	A	322	3.530	74.833	65.136	1.00	17.66	A	C
ATOM	1501	O	LEU	A	322	3.286	73.908	65.908	1.00	15.88	A	O
ATOM	1502	N	VAL	A	323	4.138	74.670	63.963	1.00	17.86	A	N
ATOM	1503	CA	VAL	A	323	4.531	73.360	63.462	1.00	19.30	A	C
ATOM	1504	CB	VAL	A	323	4.443	73.318	61.909	1.00	19.49	A	C
ATOM	1505	CG1	VAL	A	323	4.742	71.915	61.399	1.00	21.44	A	C
ATOM	1506	CG2	VAL	A	323	3.069	73.746	61.462	1.00	18.47	A	C
ATOM	1507	C	VAL	A	323	5.934	72.926	63.890	1.00	19.76	A	C
ATOM	1508	O	VAL	A	323	6.164	71.746	64.148	1.00	18.74	A	O
ATOM	1509	N	GLY	A	324	6.865	73.873	63.975	1.00	18.78	A	N
ATOM	1510	CA	GLY	A	324	8.218	73.524	64.380	1.00	19.81	A	C
ATOM	1511	C	GLY	A	324	9.219	73.717	63.257	1.00	21.90	A	C
ATOM	1512	O	GLY	A	324	10.429	73.731	63.486	1.00	23.85	A	O
ATOM	1513	N	LYS	A	325	8.715	73.851	62.034	1.00	23.08	A	N
ATOM	1514	CA	LYS	A	325	9.560	74.078	60.873	1.00	23.18	A	C
ATOM	1515	CB	LYS	A	325	10.035	72.748	60.282	1.00	25.82	A	C
ATOM	1516	CG	LYS	A	325	8.940	71.860	59.738	1.00	28.72	A	C
ATOM	1517	CD	LYS	A	325	9.550	70.690	58.988	1.00	31.14	A	C
ATOM	1518	CE	LYS	A	325	8.492	69.716	58.508	1.00	32.54	A	C
ATOM	1519	NZ	LYS	A	325	7.811	69.057	59.655	1.00	36.73	A	N
ATOM	1520	C	LYS	A	325	8.775	74.886	59.838	1.00	22.65	A	C
ATOM	1521	O	LYS	A	325	7.546	74.928	59.884	1.00	20.82	A	O
ATOM	1522	N	PRO	A	326	9.480	75.543	58.897	1.00	21.36	A	N
ATOM	1523	CD	PRO	A	326	10.936	75.420	58.702	1.00	22.88	A	C
ATOM	1524	CA	PRO	A	326	8.891	76.368	57.836	1.00	21.28	A	C
ATOM	1525	CB	PRO	A	326	10.118	76.980	57.165	1.00	23.22	A	C
ATOM	1526	CG	PRO	A	326	11.115	75.882	57.275	1.00	22.99	A	C
ATOM	1527	C	PRO	A	326	8.000	75.589	56.865	1.00	19.59	A	C
ATOM	1528	O	PRO	A	326	8.191	74.391	56.637	1.00	17.62	A	O
ATOM	1529	N	PRO	A	327	7.015	76.272	56.266	1.00	19.54	A	N

ATOM	1530	CD	PRO	A	327	6.590	77.659	56.535	1.00	18.59	A	C
ATOM	1531	CA	PRO	A	327	6.105	75.600	55.336	1.00	19.17	A	C
ATOM	1532	CB	PRO	A	327	4.946	76.594	55.212	1.00	19.31	A	C
ATOM	1533	CG	PRO	A	327	5.603	77.918	55.424	1.00	21.80	A	C
ATOM	1534	C	PRO	A	327	6.612	75.105	53.976	1.00	20.25	A	C
ATOM	1535	O	PRO	A	327	6.025	74.185	53.412	1.00	22.68	A	O
ATOM	1536	N	PHE	A	328	7.692	75.672	53.449	1.00	19.21	A	N
ATOM	1537	CA	PHE	A	328	8.179	75.244	52.134	1.00	21.50	A	C
ATOM	1538	CB	PHE	A	328	8.344	76.469	51.220	1.00	20.17	A	C
ATOM	1539	CG	PHE	A	328	7.108	77.331	51.119	1.00	19.02	A	C
ATOM	1540	CD1	PHE	A	328	5.995	76.903	50.385	1.00	19.37	A	C
ATOM	1541	CD2	PHE	A	328	7.048	78.561	51.776	1.00	17.08	A	C
ATOM	1542	CE1	PHE	A	328	4.840	77.688	50.307	1.00	16.91	A	C
ATOM	1543	CE2	PHE	A	328	5.900	79.354	51.709	1.00	20.03	A	C
ATOM	1544	CZ	PHE	A	328	4.788	78.912	50.967	1.00	18.39	A	C
ATOM	1545	C	PHE	A	328	9.501	74.466	52.163	1.00	24.45	A	C
ATOM	1546	O	PHE	A	328	10.149	74.296	51.131	1.00	24.06	A	O
ATOM	1547	N	GLU	A	329	9.902	73.992	53.337	1.00	26.19	A	N
ATOM	1548	CA	GLU	A	329	11.159	73.255	53.465	1.00	28.35	A	C
ATOM	1549	CB	GLU	A	329	11.410	72.938	54.936	1.00	31.29	A	C
ATOM	1550	CG	GLU	A	329	12.815	72.478	55.236	1.00	37.80	A	C
ATOM	1551	CD	GLU	A	329	12.954	71.963	56.648	1.00	41.63	A	C
ATOM	1552	OE1	GLU	A	329	12.396	70.880	56.938	1.00	41.71	A	O
ATOM	1553	OE2	GLU	A	329	13.614	72.646	57.468	1.00	44.04	A	O
ATOM	1554	C	GLU	A	329	11.195	71.955	52.647	1.00	27.64	A	C
ATOM	1555	O	GLU	A	329	10.230	71.193	52.639	1.00	25.94	A	O
ATOM	1556	N	ALA	A	330	12.313	71.714	51.962	1.00	26.33	A	N
ATOM	1557	CA	ALA	A	330	12.498	70.507	51.149	1.00	28.04	A	C
ATOM	1558	CB	ALA	A	330	11.948	70.731	49.731	1.00	25.92	A	C
ATOM	1559	C	ALA	A	330	13.982	70.099	51.084	1.00	28.74	A	C
ATOM	1560	O	ALA	A	330	14.856	70.838	51.537	1.00	29.37	A	O
ATOM	1561	N	ASN	A	331	14.259	68.930	50.513	1.00	30.23	A	N
ATOM	1562	CA	ASN	A	331	15.627	68.421	50.411	1.00	31.60	A	C
ATOM	1563	CB	ASN	A	331	15.610	66.949	50.002	1.00	34.66	A	C
ATOM	1564	CG	ASN	A	331	14.955	66.069	51.041	1.00	38.24	A	C
ATOM	1565	OD1	ASN	A	331	15.440	65.949	52.165	1.00	39.85	A	O
ATOM	1566	ND2	ASN	A	331	13.841	65.449	50.672	1.00	42.35	A	N
ATOM	1567	C	ASN	A	331	16.532	69.189	49.459	1.00	31.72	A	C
ATOM	1568	O	ASN	A	331	17.757	69.115	49.572	1.00	31.03	A	O
ATOM	1569	N	THR	A	332	15.946	69.918	48.512	1.00	31.48	A	N
ATOM	1570	CA	THR	A	332	16.756	70.684	47.566	1.00	29.77	A	C
ATOM	1571	CB	THR	A	332	16.799	70.011	46.173	1.00	28.89	A	C
ATOM	1572	OG1	THR	A	332	15.487	70.003	45.606	1.00	29.21	A	O
ATOM	1573	CG2	THR	A	332	17.308	68.580	46.279	1.00	27.84	A	C
ATOM	1574	C	THR	A	332	16.270	72.118	47.383	1.00	31.57	A	C
ATOM	1575	O	THR	A	332	15.093	72.433	47.603	1.00	30.47	A	O
ATOM	1576	N	TYR	A	333	17.202	72.981	46.990	1.00	30.46	A	N
ATOM	1577	CA	TYR	A	333	16.918	74.386	46.744	1.00	32.40	A	C
ATOM	1578	CB	TYR	A	333	18.187	75.094	46.254	1.00	35.27	A	C
ATOM	1579	CG	TYR	A	333	19.283	75.216	47.286	1.00	39.94	A	C
ATOM	1580	CD1	TYR	A	333	20.620	75.025	46.934	1.00	41.64	A	C
ATOM	1581	CE1	TYR	A	333	21.640	75.157	47.874	1.00	43.08	A	C
ATOM	1582	CD2	TYR	A	333	18.992	75.542	48.608	1.00	40.76	A	C
ATOM	1583	CE2	TYR	A	333	20.007	75.677	49.555	1.00	43.70	A	C
ATOM	1584	CZ	TYR	A	333	21.323	75.483	49.178	1.00	43.66	A	C
ATOM	1585	OH	TYR	A	333	22.323	75.613	50.107	1.00	47.82	A	O
ATOM	1586	C	TYR	A	333	15.842	74.529	45.671	1.00	31.07	A	C
ATOM	1587	O	TYR	A	333	14.916	75.327	45.807	1.00	31.04	A	O
ATOM	1588	N	GLN	A	334	15.991	73.754	44.601	1.00	29.99	A	N
ATOM	1589	CA	GLN	A	334	15.069	73.778	43.471	1.00	30.74	A	C
ATOM	1590	CB	GLN	A	334	15.526	72.779	42.403	1.00	33.77	A	C
ATOM	1591	CG	GLN	A	334	14.434	72.304	41.439	1.00	41.43	A	C
ATOM	1592	CD	GLN	A	334	13.963	73.367	40.443	1.00	46.44	A	C
ATOM	1593	OE1	GLN	A	334	13.366	74.388	40.820	1.00	47.38	A	O
ATOM	1594	NE2	GLN	A	334	14.222	73.120	39.156	1.00	47.54	A	N
ATOM	1595	C	GLN	A	334	13.639	73.480	43.878	1.00	27.78	A	C
ATOM	1596	O	GLN	A	334	12.725	74.204	43.504	1.00	26.99	A	O
ATOM	1597	N	GLU	A	335	13.448	72.412	44.641	1.00	26.65	A	N
ATOM	1598	CA	GLU	A	335	12.114	72.041	45.085	1.00	26.25	A	C
ATOM	1599	CB	GLU	A	335	12.158	70.678	45.785	1.00	29.22	A	C
ATOM	1600	CG	GLU	A	335	10.814	70.193	46.294	1.00	34.80	A	C
ATOM	1601	CD	GLU	A	335	9.755	70.092	45.197	1.00	39.80	A	C

ATOM	1602	OE1	GLU	A	335	8.569	69.866	45.539	1.00	41.99	A	O
ATOM	1603	OE2	GLU	A	335	10.101	70.231	43.999	1.00	40.49	A	O
ATOM	1604	C	GLU	A	335	11.502	73.108	46.005	1.00	23.81	A	C
ATOM	1605	O	GLU	A	335	10.295	73.333	45.969	1.00	22.15	A	O
ATOM	1606	N	THR	A	336	12.332	73.781	46.802	1.00	21.23	A	N
ATOM	1607	CA	THR	A	336	11.835	74.821	47.710	1.00	21.06	A	C
ATOM	1608	CB	THR	A	336	12.911	75.253	48.723	1.00	20.94	A	C
ATOM	1609	OG1	THR	A	336	13.207	74.155	49.593	1.00	21.30	A	O
ATOM	1610	CG2	THR	A	336	12.418	76.430	49.561	1.00	19.68	A	C
ATOM	1611	C	THR	A	336	11.375	76.036	46.920	1.00	21.05	A	C
ATOM	1612	O	THR	A	336	10.317	76.634	47.204	1.00	19.51	A	O
ATOM	1613	N	TYR	A	337	12.177	76.386	45.921	1.00	22.32	A	N
ATOM	1614	CA	TYR	A	337	11.888	77.500	45.026	1.00	23.61	A	C
ATOM	1615	CB	TYR	A	337	12.987	77.601	43.959	1.00	28.60	A	C
ATOM	1616	CG	TYR	A	337	12.727	78.643	42.890	1.00	35.53	A	C
ATOM	1617	CD1	TYR	A	337	13.096	79.978	43.076	1.00	38.47	A	C
ATOM	1618	CE1	TYR	A	337	12.825	80.947	42.100	1.00	41.00	A	C
ATOM	1619	CD2	TYR	A	337	12.081	78.298	41.700	1.00	38.75	A	C
ATOM	1620	CE2	TYR	A	337	11.803	79.251	40.722	1.00	41.63	A	C
ATOM	1621	CZ	TYR	A	337	12.177	80.573	40.927	1.00	43.73	A	C
ATOM	1622	OH	TYR	A	337	11.890	81.513	39.958	1.00	46.53	A	O
ATOM	1623	C	TYR	A	337	10.546	77.221	44.346	1.00	22.77	A	C
ATOM	1624	O	TYR	A	337	9.680	78.096	44.261	1.00	20.90	A	O
ATOM	1625	N	LYS	A	338	10.384	75.988	43.870	1.00	22.05	A	N
ATOM	1626	CA	LYS	A	338	9.163	75.578	43.183	1.00	24.06	A	C
ATOM	1627	CB	LYS	A	338	9.314	74.153	42.633	1.00	28.55	A	C
ATOM	1628	CG	LYS	A	338	8.183	73.729	41.703	1.00	35.30	A	C
ATOM	1629	CD	LYS	A	338	8.152	72.221	41.440	1.00	41.29	A	C
ATOM	1630	CE	LYS	A	338	9.451	71.691	40.831	1.00	42.96	A	C
ATOM	1631	NZ	LYS	A	338	10.551	71.612	41.836	1.00	45.52	A	N
ATOM	1632	C	LYS	A	338	7.934	75.656	44.094	1.00	22.36	A	C
ATOM	1633	O	LYS	A	338	6.894	76.160	43.686	1.00	22.23	A	O
ATOM	1634	N	ARG	A	339	8.056	75.174	45.328	1.00	20.86	A	N
ATOM	1635	CA	ARG	A	339	6.936	75.214	46.263	1.00	19.98	A	C
ATOM	1636	CB	ARG	A	339	7.252	74.388	47.506	1.00	21.06	A	C
ATOM	1637	CG	ARG	A	339	7.288	72.892	47.250	1.00	24.15	A	C
ATOM	1638	CD	ARG	A	339	7.637	72.141	48.504	1.00	25.25	A	C
ATOM	1639	NE	ARG	A	339	7.821	70.720	48.241	1.00	30.16	A	N
ATOM	1640	CZ	ARG	A	339	8.053	69.811	49.182	1.00	30.16	A	C
ATOM	1641	NH1	ARG	A	339	8.126	70.173	50.456	1.00	31.69	A	N
ATOM	1642	NH2	ARG	A	339	8.217	68.541	48.848	1.00	32.15	A	N
ATOM	1643	C	ARG	A	339	6.516	76.626	46.685	1.00	17.94	A	C
ATOM	1644	O	ARG	A	339	5.339	76.878	46.919	1.00	14.93	A	O
ATOM	1645	N	ILE	A	340	7.478	77.536	46.788	1.00	17.04	A	N
ATOM	1646	CA	ILE	A	340	7.187	78.908	47.175	1.00	16.76	A	C
ATOM	1647	CB	ILE	A	340	8.497	79.705	47.480	1.00	14.52	A	C
ATOM	1648	CG2	ILE	A	340	8.203	81.199	47.598	1.00	14.90	A	C
ATOM	1649	CG1	ILE	A	340	9.127	79.209	48.786	1.00	14.96	A	C
ATOM	1650	CD1	ILE	A	340	10.491	79.833	49.095	1.00	16.04	A	C
ATOM	1651	C	ILE	A	340	6.433	79.573	46.030	1.00	16.16	A	C
ATOM	1652	O	ILE	A	340	5.369	80.139	46.225	1.00	16.78	A	O
ATOM	1653	N	SER	A	341	6.988	79.469	44.829	1.00	18.02	A	N
ATOM	1654	CA	SER	A	341	6.397	80.061	43.636	1.00	19.89	A	C
ATOM	1655	CB	SER	A	341	7.302	79.792	42.423	1.00	22.71	A	C
ATOM	1656	OG	SER	A	341	6.820	80.457	41.269	1.00	27.61	A	O
ATOM	1657	C	SER	A	341	4.982	79.552	43.360	1.00	19.31	A	C
ATOM	1658	O	SER	A	341	4.118	80.318	42.946	1.00	18.97	A	O
ATOM	1659	N	ARG	A	342	4.753	78.262	43.594	1.00	19.76	A	N
ATOM	1660	CA	ARG	A	342	3.443	77.658	43.382	1.00	21.30	A	C
ATOM	1661	CB	ARG	A	342	3.597	76.214	42.911	1.00	24.17	A	C
ATOM	1662	CG	ARG	A	342	4.204	76.121	41.531	1.00	26.81	A	C
ATOM	1663	CD	ARG	A	342	4.268	74.702	41.017	1.00	31.06	A	C
ATOM	1664	NE	ARG	A	342	4.686	74.692	39.617	1.00	35.62	A	N
ATOM	1665	CZ	ARG	A	342	4.769	73.601	38.868	1.00	36.48	A	C
ATOM	1666	NH1	ARG	A	342	5.157	73.700	37.606	1.00	40.12	A	N
ATOM	1667	NH2	ARG	A	342	4.471	72.414	39.382	1.00	38.88	A	N
ATOM	1668	C	ARG	A	342	2.580	77.690	44.634	1.00	21.34	A	C
ATOM	1669	O	ARG	A	342	1.403	77.298	44.600	1.00	21.22	A	O
ATOM	1670	N	VAL	A	343	3.173	78.165	45.729	1.00	19.64	A	N
ATOM	1671	CA	VAL	A	343	2.499	78.260	47.022	1.00	19.20	A	C
ATOM	1672	CB	VAL	A	343	1.386	79.323	47.000	1.00	18.65	A	C
ATOM	1673	CG1	VAL	A	343	0.848	79.534	48.417	1.00	15.93	A	C

ATOM	1674	CG2	VAL	A	343	1.920	80.622	46.410	1.00	17.93	A	C
ATOM	1675	C	VAL	A	343	1.887	76.917	47.403	1.00	19.26	A	C
ATOM	1676	O	VAL	A	343	0.667	76.793	47.569	1.00	19.70	A	O
ATOM	1677	N	GLU	A	344	2.747	75.916	47.544	1.00	17.68	A	N
ATOM	1678	CA	GLU	A	344	2.311	74.568	47.879	1.00	19.81	A	C
ATOM	1679	CB	GLU	A	344	2.860	73.584	46.830	1.00	19.99	A	C
ATOM	1680	CG	GLU	A	344	2.339	73.871	45.426	1.00	26.77	A	C
ATOM	1681	CD	GLU	A	344	3.088	73.125	44.328	1.00	29.54	A	C
ATOM	1682	OE1	GLU	A	344	2.646	73.198	43.163	1.00	33.31	A	O
ATOM	1683	OE2	GLU	A	344	4.115	72.476	44.619	1.00	30.95	A	O
ATOM	1684	C	GLU	A	344	2.738	74.142	49.277	1.00	19.23	A	C
ATOM	1685	O	GLU	A	344	3.928	73.915	49.529	1.00	17.01	A	O
ATOM	1686	N	PHE	A	345	1.763	74.038	50.184	1.00	18.09	A	N
ATOM	1687	CA	PHE	A	345	2.030	73.621	51.555	1.00	19.56	A	C
ATOM	1688	CB	PHE	A	345	2.529	74.811	52.410	1.00	18.38	A	C
ATOM	1689	CG	PHE	A	345	1.461	75.833	52.734	1.00	18.52	A	C
ATOM	1690	CD1	PHE	A	345	0.592	75.644	53.810	1.00	21.05	A	C
ATOM	1691	CD2	PHE	A	345	1.313	76.982	51.951	1.00	18.65	A	C
ATOM	1692	CE1	PHE	A	345	-0.415	76.584	54.102	1.00	16.74	A	C
ATOM	1693	CE2	PHE	A	345	0.310	77.925	52.235	1.00	19.55	A	C
ATOM	1694	CZ	PHE	A	345	-0.553	77.720	53.317	1.00	18.36	A	C
ATOM	1695	C	PHE	A	345	0.779	73.033	52.185	1.00	20.33	A	C
ATOM	1696	O	PHE	A	345	-0.332	73.277	51.708	1.00	20.11	A	O
ATOM	1697	N	THR	A	346	0.952	72.260	53.255	1.00	19.73	A	N
ATOM	1698	CA	THR	A	346	-0.136	71.655	53.985	1.00	19.58	A	C
ATOM	1699	CB	THR	A	346	-0.326	70.158	53.615	1.00	20.72	A	C
ATOM	1700	OG1	THR	A	346	0.916	69.459	53.746	1.00	20.60	A	O
ATOM	1701	CG2	THR	A	346	-0.821	70.023	52.177	1.00	20.25	A	C
ATOM	1702	C	THR	A	346	0.116	71.792	55.487	1.00	20.13	A	C
ATOM	1703	O	THR	A	346	1.232	72.103	55.902	1.00	18.25	A	O
ATOM	1704	N	PHE	A	347	-0.932	71.567	56.282	1.00	20.15	A	N
ATOM	1705	CA	PHE	A	347	-0.887	71.673	57.746	1.00	20.73	A	C
ATOM	1706	CB	PHE	A	347	-2.084	72.476	58.280	1.00	19.55	A	C
ATOM	1707	CG	PHE	A	347	-2.217	73.870	57.720	1.00	20.41	A	C
ATOM	1708	CD1	PHE	A	347	-1.433	74.909	58.201	1.00	17.74	A	C
ATOM	1709	CD2	PHE	A	347	-3.178	74.150	56.744	1.00	20.45	A	C
ATOM	1710	CE1	PHE	A	347	-1.597	76.204	57.732	1.00	18.97	A	C
ATOM	1711	CE2	PHE	A	347	-3.354	75.449	56.264	1.00	19.38	A	C
ATOM	1712	CZ	PHE	A	347	-2.566	76.476	56.757	1.00	20.54	A	C
ATOM	1713	C	PHE	A	347	-0.983	70.309	58.430	1.00	22.46	A	C
ATOM	1714	O	PHE	A	347	-1.685	69.416	57.952	1.00	21.99	A	O
ATOM	1715	N	PRO	A	348	-0.285	70.133	59.565	1.00	24.54	A	N
ATOM	1716	CD	PRO	A	348	0.801	70.979	60.093	1.00	25.31	A	C
ATOM	1717	CA	PRO	A	348	-0.354	68.854	60.286	1.00	23.76	A	C
ATOM	1718	CB	PRO	A	348	0.728	68.991	61.354	1.00	24.65	A	C
ATOM	1719	CG	PRO	A	348	1.715	69.961	60.728	1.00	26.35	A	C
ATOM	1720	C	PRO	A	348	-1.756	68.822	60.910	1.00	24.94	A	C
ATOM	1721	O	PRO	A	348	-2.389	69.868	61.056	1.00	22.13	A	O
ATOM	1722	N	ASP	A	349	-2.231	67.640	61.286	1.00	27.34	A	N
ATOM	1723	CA	ASP	A	349	-3.568	67.503	61.870	1.00	30.19	A	C
ATOM	1724	CB	ASP	A	349	-3.856	66.047	62.234	1.00	33.25	A	C
ATOM	1725	CG	ASP	A	349	-3.804	65.139	61.045	1.00	37.28	A	C
ATOM	1726	OD1	ASP	A	349	-4.341	65.526	59.987	1.00	39.75	A	O
ATOM	1727	OD2	ASP	A	349	-3.232	64.034	61.172	1.00	41.94	A	O
ATOM	1728	C	ASP	A	349	-3.856	68.342	63.103	1.00	30.17	A	C
ATOM	1729	O	ASP	A	349	-4.987	68.777	63.293	1.00	29.70	A	O
ATOM	1730	N	PHE	A	350	-2.855	68.565	63.949	1.00	28.31	A	N
ATOM	1731	CA	PHE	A	350	-3.100	69.334	65.160	1.00	26.49	A	C
ATOM	1732	CB	PHE	A	350	-1.977	69.094	66.184	1.00	25.79	A	C
ATOM	1733	CG	PHE	A	350	-0.600	69.470	65.705	1.00	24.86	A	C
ATOM	1734	CD1	PHE	A	350	-0.183	70.798	65.703	1.00	27.41	A	C
ATOM	1735	CD2	PHE	A	350	0.294	68.492	65.296	1.00	22.65	A	C
ATOM	1736	CE1	PHE	A	350	1.112	71.143	65.302	1.00	23.41	A	C
ATOM	1737	CE2	PHE	A	350	1.586	68.824	64.895	1.00	22.60	A	C
ATOM	1738	CZ	PHE	A	350	1.995	70.153	64.899	1.00	23.36	A	C
ATOM	1739	C	PHE	A	350	-3.349	70.830	64.963	1.00	26.28	A	C
ATOM	1740	O	PHE	A	350	-3.926	71.482	65.833	1.00	26.14	A	O
ATOM	1741	N	VAL	A	351	-2.957	71.380	63.820	1.00	24.56	A	N
ATOM	1742	CA	VAL	A	351	-3.174	72.809	63.600	1.00	23.91	A	C
ATOM	1743	CB	VAL	A	351	-2.429	73.304	62.341	1.00	21.91	A	C
ATOM	1744	CG1	VAL	A	351	-2.624	74.803	62.184	1.00	22.59	A	C
ATOM	1745	CG2	VAL	A	351	-0.943	72.989	62.459	1.00	19.79	A	C

ATOM	1746	C	VAL	A	351	-4.666	73.183	63.510	1.00	23.38	A	C
ATOM	1747	O	VAL	A	351	-5.408	72.635	62.707	1.00	23.52	A	O
ATOM	1748	N	THR	A	352	-5.076	74.123	64.358	1.00	23.53	A	N
ATOM	1749	CA	THR	A	352	-6.454	74.618	64.463	1.00	24.90	A	C
ATOM	1750	CB	THR	A	352	-6.561	75.531	65.724	1.00	26.17	A	C
ATOM	1751	OG1	THR	A	352	-6.461	74.713	66.893	1.00	29.32	A	O
ATOM	1752	CG2	THR	A	352	-7.872	76.284	65.769	1.00	31.36	A	C
ATOM	1753	C	THR	A	352	-7.013	75.350	63.230	1.00	23.73	A	C
ATOM	1754	O	THR	A	352	-6.270	75.946	62.447	1.00	23.43	A	O
ATOM	1755	N	GLU	A	353	-8.335	75.306	63.059	1.00	24.62	A	N
ATOM	1756	CA	GLU	A	353	-8.967	75.954	61.909	1.00	24.68	A	C
ATOM	1757	CB	GLU	A	353	-10.468	75.643	61.869	1.00	29.50	A	C
ATOM	1758	CG	GLU	A	353	-10.797	74.232	61.368	1.00	35.19	A	C
ATOM	1759	CD	GLU	A	353	-10.272	73.983	59.966	1.00	38.71	A	C
ATOM	1760	OE1	GLU	A	353	-10.401	74.895	59.117	1.00	40.65	A	O
ATOM	1761	OE2	GLU	A	353	-9.739	72.879	59.703	1.00	40.38	A	O
ATOM	1762	C	GLU	A	353	-8.752	77.464	61.858	1.00	21.70	A	C
ATOM	1763	O	GLU	A	353	-8.583	78.041	60.782	1.00	19.58	A	O
ATOM	1764	N	GLY	A	354	-8.755	78.106	63.017	1.00	19.06	A	N
ATOM	1765	CA	GLY	A	354	-8.551	79.542	63.035	1.00	17.79	A	C
ATOM	1766	C	GLY	A	354	-7.128	79.867	62.603	1.00	18.40	A	C
ATOM	1767	O	GLY	A	354	-6.878	80.874	61.930	1.00	16.97	A	O
ATOM	1768	N	ALA	A	355	-6.191	79.009	62.993	1.00	14.57	A	N
ATOM	1769	CA	ALA	A	355	-4.794	79.210	62.648	1.00	15.46	A	C
ATOM	1770	CB	ALA	A	355	-3.919	78.229	63.439	1.00	16.64	A	C
ATOM	1771	C	ALA	A	355	-4.589	79.038	61.136	1.00	14.00	A	C
ATOM	1772	O	ALA	A	355	-3.846	79.800	60.508	1.00	10.53	A	O
ATOM	1773	N	ARG	A	356	-5.269	78.043	60.565	1.00	15.01	A	N
ATOM	1774	CA	ARG	A	356	-5.199	77.759	59.133	1.00	16.46	A	C
ATOM	1775	CB	ARG	A	356	-6.010	76.503	58.799	1.00	16.70	A	C
ATOM	1776	CG	ARG	A	356	-5.460	75.229	59.389	1.00	18.49	A	C
ATOM	1777	CD	ARG	A	356	-6.495	74.120	59.378	1.00	22.62	A	C
ATOM	1778	NE	ARG	A	356	-6.108	73.006	58.518	1.00	28.84	A	N
ATOM	1779	CZ	ARG	A	356	-5.911	71.762	58.945	1.00	29.04	A	C
ATOM	1780	NH1	ARG	A	356	-6.058	71.463	60.224	1.00	27.32	A	N
ATOM	1781	NH2	ARG	A	356	-5.577	70.811	58.086	1.00	31.07	A	N
ATOM	1782	C	ARG	A	356	-5.758	78.941	58.350	1.00	15.08	A	C
ATOM	1783	O	ARG	A	356	-5.225	79.335	57.319	1.00	14.99	A	O
ATOM	1784	N	ASP	A	357	-6.815	79.508	58.860	1.00	18.02	A	N
ATOM	1785	CA	ASP	A	357	-7.466	80.646	58.214	1.00	18.90	A	C
ATOM	1786	CB	ASP	A	357	-8.694	81.096	58.994	1.00	18.88	A	C
ATOM	1787	CG	ASP	A	357	-9.406	82.240	58.312	1.00	22.28	A	C
ATOM	1788	OD1	ASP	A	357	-9.966	81.992	57.235	1.00	22.61	A	O
ATOM	1789	OD2	ASP	A	357	-9.388	83.381	58.830	1.00	24.45	A	O
ATOM	1790	C	ASP	A	357	-6.489	81.824	58.092	1.00	19.84	A	C
ATOM	1791	O	ASP	A	357	-6.289	82.342	56.998	1.00	20.32	A	O
ATOM	1792	N	LEU	A	358	-5.900	82.238	59.211	1.00	18.05	A	N
ATOM	1793	CA	LEU	A	358	-4.942	83.358	59.219	1.00	18.23	A	C
ATOM	1794	CB	LEU	A	358	-4.411	83.613	60.638	1.00	18.23	A	C
ATOM	1795	CG	LEU	A	358	-3.394	84.760	60.758	1.00	20.75	A	C
ATOM	1796	CD1	LEU	A	358	-4.012	86.056	60.216	1.00	19.09	A	C
ATOM	1797	CD2	LEU	A	358	-2.964	84.934	62.208	1.00	17.47	A	C
ATOM	1798	C	LEU	A	358	-3.749	83.145	58.290	1.00	16.19	A	C
ATOM	1799	O	LEU	A	358	-3.413	84.021	57.481	1.00	16.52	A	O
ATOM	1800	N	ILE	A	359	-3.119	81.983	58.415	1.00	15.38	A	N
ATOM	1801	CA	ILE	A	359	-1.956	81.629	57.613	1.00	16.57	A	C
ATOM	1802	CB	ILE	A	359	-1.329	80.296	58.114	1.00	16.35	A	C
ATOM	1803	CG2	ILE	A	359	-0.186	79.879	57.193	1.00	13.83	A	C
ATOM	1804	CG1	ILE	A	359	-0.825	80.469	59.553	1.00	17.25	A	C
ATOM	1805	CD1	ILE	A	359	-0.321	79.200	60.220	1.00	14.18	A	C
ATOM	1806	C	ILE	A	359	-2.255	81.518	56.112	1.00	17.80	A	C
ATOM	1807	O	ILE	A	359	-1.398	81.829	55.294	1.00	18.14	A	O
ATOM	1808	N	SER	A	360	-3.464	81.079	55.759	1.00	19.68	A	N
ATOM	1809	CA	SER	A	360	-3.867	80.938	54.354	1.00	21.20	A	C
ATOM	1810	CB	SER	A	360	-5.153	80.099	54.233	1.00	19.64	A	C
ATOM	1811	OG	SER	A	360	-4.950	78.757	54.649	1.00	20.82	A	O
ATOM	1812	C	SER	A	360	-4.105	82.303	53.714	1.00	22.33	A	C
ATOM	1813	O	SER	A	360	-3.958	82.467	52.501	1.00	20.61	A	O
ATOM	1814	N	ARG	A	361	-4.500	83.274	54.533	1.00	23.60	A	N
ATOM	1815	CA	ARG	A	361	-4.741	84.633	54.059	1.00	23.75	A	C
ATOM	1816	CB	ARG	A	361	-5.587	85.410	55.072	1.00	28.01	A	C
ATOM	1817	CG	ARG	A	361	-7.078	85.081	55.087	1.00	32.71	A	C

ATOM	1818	CD	ARG	A	361	-7.726	85.333	53.723	1.00	39.20	A	C
ATOM	1819	NE	ARG	A	361	-7.187	86.514	53.042	1.00	44.85	A	N
ATOM	1820	CZ	ARG	A	361	-7.332	87.772	53.456	1.00	46.87	A	C
ATOM	1821	NH1	ARG	A	361	-8.012	88.048	54.562	1.00	45.54	A	N
ATOM	1822	NH2	ARG	A	361	-6.772	88.759	52.767	1.00	47.53	A	N
ATOM	1823	C	ARG	A	361	-3.414	85.369	53.863	1.00	21.60	A	C
ATOM	1824	O	ARG	A	361	-3.268	86.174	52.941	1.00	24.02	A	O
ATOM	1825	N	LEU	A	362	-2.450	85.078	54.730	1.00	19.99	A	N
ATOM	1826	CA	LEU	A	362	-1.139	85.730	54.683	1.00	18.01	A	C
ATOM	1827	CB	LEU	A	362	-0.431	85.627	56.042	1.00	15.49	A	C
ATOM	1828	CG	LEU	A	362	-0.993	86.459	57.207	1.00	15.69	A	C
ATOM	1829	CD1	LEU	A	362	-0.312	86.063	58.496	1.00	10.97	A	C
ATOM	1830	CD2	LEU	A	362	-0.801	87.948	56.941	1.00	15.65	A	C
ATOM	1831	C	LEU	A	362	-0.225	85.192	53.603	1.00	18.43	A	C
ATOM	1832	O	LEU	A	362	0.608	85.930	53.080	1.00	18.21	A	O
ATOM	1833	N	LEU	A	363	-0.362	83.911	53.271	1.00	19.92	A	N
ATOM	1834	CA	LEU	A	363	0.483	83.328	52.235	1.00	21.77	A	C
ATOM	1835	CB	LEU	A	363	0.918	81.910	52.623	1.00	21.94	A	C
ATOM	1836	CG	LEU	A	363	1.412	81.704	54.065	1.00	26.68	A	C
ATOM	1837	CD1	LEU	A	363	2.276	80.444	54.158	1.00	23.94	A	C
ATOM	1838	CD2	LEU	A	363	2.215	82.925	54.518	1.00	26.76	A	C
ATOM	1839	C	LEU	A	363	-0.243	83.314	50.892	1.00	22.91	A	C
ATOM	1840	O	LEU	A	363	-0.570	82.261	50.359	1.00	24.15	A	O
ATOM	1841	N	LYS	A	364	-0.505	84.508	50.370	1.00	23.56	A	N
ATOM	1842	CA	LYS	A	364	-1.180	84.691	49.090	1.00	23.34	A	C
ATOM	1843	CB	LYS	A	364	-2.211	85.818	49.181	1.00	24.62	A	C
ATOM	1844	CG	LYS	A	364	-3.545	85.423	49.806	1.00	26.87	A	C
ATOM	1845	CD	LYS	A	364	-4.289	84.446	48.912	1.00	29.10	A	C
ATOM	1846	CE	LYS	A	364	-5.713	84.208	49.392	1.00	32.69	A	C
ATOM	1847	NZ	LYS	A	364	-6.503	83.427	48.391	1.00	32.47	A	N
ATOM	1848	C	LYS	A	364	-0.144	85.052	48.032	1.00	22.89	A	C
ATOM	1849	O	LYS	A	364	0.696	85.929	48.247	1.00	23.81	A	O
ATOM	1850	N	HIS	A	365	-0.210	84.375	46.893	1.00	22.71	A	N
ATOM	1851	CA	HIS	A	365	0.717	84.624	45.797	1.00	23.97	A	C
ATOM	1852	CB	HIS	A	365	0.380	83.734	44.602	1.00	24.15	A	C
ATOM	1853	CG	HIS	A	365	1.275	83.955	43.426	1.00	25.26	A	C
ATOM	1854	CD2	HIS	A	365	1.097	84.673	42.293	1.00	26.54	A	C
ATOM	1855	ND1	HIS	A	365	2.563	83.470	43.372	1.00	27.83	A	N
ATOM	1856	CE1	HIS	A	365	3.142	83.883	42.258	1.00	26.33	A	C
ATOM	1857	NE2	HIS	A	365	2.274	84.617	41.588	1.00	26.94	A	N
ATOM	1858	C	HIS	A	365	0.703	86.085	45.354	1.00	23.66	A	C
ATOM	1859	O	HIS	A	365	1.757	86.695	45.187	1.00	24.80	A	O
ATOM	1860	N	ASN	A	366	-0.491	86.631	45.144	1.00	25.39	A	N
ATOM	1861	CA	ASN	A	366	-0.667	88.027	44.729	1.00	28.27	A	C
ATOM	1862	CB	ASN	A	366	-2.058	88.197	44.101	1.00	30.44	A	C
ATOM	1863	CG	ASN	A	366	-2.331	89.620	43.624	1.00	33.56	A	C
ATOM	1864	OD1	ASN	A	366	-3.386	89.895	43.051	1.00	36.37	A	O
ATOM	1865	ND2	ASN	A	366	-1.390	90.525	43.857	1.00	32.69	A	N
ATOM	1866	C	ASN	A	366	-0.526	88.926	45.965	1.00	28.67	A	C
ATOM	1867	O	ASN	A	366	-1.389	88.928	46.843	1.00	29.64	A	O
ATOM	1868	N	PRO	A	367	0.562	89.706	46.044	1.00	29.87	A	N
ATOM	1869	CD	PRO	A	367	1.612	89.829	45.019	1.00	28.83	A	C
ATOM	1870	CA	PRO	A	367	0.832	90.611	47.172	1.00	31.07	A	C
ATOM	1871	CB	PRO	A	367	2.013	91.437	46.675	1.00	30.37	A	C
ATOM	1872	CG	PRO	A	367	2.734	90.479	45.790	1.00	30.85	A	C
ATOM	1873	C	PRO	A	367	-0.328	91.496	47.624	1.00	32.07	A	C
ATOM	1874	O	PRO	A	367	-0.483	91.754	48.820	1.00	32.30	A	O
ATOM	1875	N	SER	A	368	-1.131	91.966	46.671	1.00	32.61	A	N
ATOM	1876	CA	SER	A	368	-2.261	92.834	46.987	1.00	34.50	A	C
ATOM	1877	CB	SER	A	368	-2.760	93.547	45.720	1.00	35.81	A	C
ATOM	1878	OG	SER	A	368	-3.206	92.623	44.736	1.00	36.05	A	O
ATOM	1879	C	SER	A	368	-3.413	92.088	47.656	1.00	35.02	A	C
ATOM	1880	O	SER	A	368	-4.290	92.706	48.258	1.00	37.52	A	O
ATOM	1881	N	GLN	A	369	-3.418	90.763	47.554	1.00	34.24	A	N
ATOM	1882	CA	GLN	A	369	-4.475	89.975	48.176	1.00	33.87	A	C
ATOM	1883	CB	GLN	A	369	-4.644	88.637	47.463	1.00	36.07	A	C
ATOM	1884	CG	GLN	A	369	-5.499	88.695	46.218	1.00	40.88	A	C
ATOM	1885	CD	GLN	A	369	-5.478	87.382	45.463	1.00	44.11	A	C
ATOM	1886	OE1	GLN	A	369	-5.619	86.308	46.059	1.00	45.39	A	O
ATOM	1887	NE2	GLN	A	369	-5.303	87.457	44.145	1.00	45.10	A	N
ATOM	1888	C	GLN	A	369	-4.214	89.721	49.653	1.00	32.42	A	C
ATOM	1889	O	GLN	A	369	-5.045	89.136	50.336	1.00	31.67	A	O

ATOM	1890	N	ARG	A	370	-3.053	90.149	50.141	1.00	31.86	A	N
ATOM	1891	CA	ARG	A	370	-2.714	89.968	51.549	1.00	30.59	A	C
ATOM	1892	CB	ARG	A	370	-1.193	89.979	51.741	1.00	27.86	A	C
ATOM	1893	CG	ARG	A	370	-0.498	88.834	51.047	1.00	27.06	A	C
ATOM	1894	CD	ARG	A	370	1.015	89.020	50.987	1.00	25.62	A	C
ATOM	1895	NE	ARG	A	370	1.552	88.214	49.901	1.00	23.24	A	N
ATOM	1896	CZ	ARG	A	370	2.744	88.385	49.344	1.00	22.14	A	C
ATOM	1897	NH1	ARG	A	370	3.557	89.340	49.777	1.00	19.46	A	N
ATOM	1898	NH2	ARG	A	370	3.098	87.618	48.314	1.00	20.24	A	N
ATOM	1899	C	ARG	A	370	-3.349	91.103	52.344	1.00	30.03	A	C
ATOM	1900	O	ARG	A	370	-3.380	92.244	51.887	1.00	30.03	A	O
ATOM	1901	N	PRO	A	371	-3.861	90.801	53.549	1.00	29.42	A	N
ATOM	1902	CD	PRO	A	371	-3.861	89.468	54.180	1.00	28.61	A	C
ATOM	1903	CA	PRO	A	371	-4.506	91.783	54.426	1.00	29.38	A	C
ATOM	1904	CB	PRO	A	371	-5.105	90.911	55.524	1.00	28.93	A	C
ATOM	1905	CG	PRO	A	371	-4.130	89.800	55.626	1.00	27.39	A	C
ATOM	1906	C	PRO	A	371	-3.579	92.856	54.995	1.00	30.07	A	C
ATOM	1907	O	PRO	A	371	-2.356	92.719	54.979	1.00	30.66	A	O
ATOM	1908	N	MET	A	372	-4.179	93.932	55.489	1.00	29.01	A	N
ATOM	1909	CA	MET	A	372	-3.422	95.014	56.095	1.00	28.79	A	C
ATOM	1910	CB	MET	A	372	-4.297	96.255	56.209	1.00	32.05	A	C
ATOM	1911	CG	MET	A	372	-4.983	96.641	54.909	1.00	38.91	A	C
ATOM	1912	SD	MET	A	372	-6.339	97.820	55.165	1.00	45.86	A	S
ATOM	1913	CE	MET	A	372	-5.396	99.295	55.623	1.00	43.73	A	C
ATOM	1914	C	MET	A	372	-3.050	94.511	57.484	1.00	27.02	A	C
ATOM	1915	O	MET	A	372	-3.635	93.542	57.965	1.00	25.83	A	O
ATOM	1916	N	LEU	A	373	-2.084	95.160	58.126	1.00	26.03	A	N
ATOM	1917	CA	LEU	A	373	-1.650	94.759	59.462	1.00	24.32	A	C
ATOM	1918	CB	LEU	A	373	-0.422	95.570	59.886	1.00	24.26	A	C
ATOM	1919	CG	LEU	A	373	0.874	95.259	59.134	1.00	24.53	A	C
ATOM	1920	CD1	LEU	A	373	1.971	96.239	59.545	1.00	22.42	A	C
ATOM	1921	CD2	LEU	A	373	1.291	93.821	59.422	1.00	22.22	A	C
ATOM	1922	C	LEU	A	373	-2.756	94.910	60.504	1.00	23.93	A	C
ATOM	1923	O	LEU	A	373	-2.789	94.181	61.488	1.00	24.38	A	O
ATOM	1924	N	ALA	A	374	-3.666	95.852	60.281	1.00	24.38	A	N
ATOM	1925	CA	ALA	A	374	-4.772	96.080	61.203	1.00	22.71	A	C
ATOM	1926	CB	ALA	A	374	-5.503	97.370	60.836	1.00	26.79	A	C
ATOM	1927	C	ALA	A	374	-5.741	94.911	61.164	1.00	23.14	A	C
ATOM	1928	O	ALA	A	374	-6.432	94.637	62.150	1.00	22.46	A	O
ATOM	1929	N	GLU	A	375	-5.798	94.227	60.022	1.00	23.02	A	N
ATOM	1930	CA	GLU	A	375	-6.694	93.084	59.875	1.00	25.10	A	C
ATOM	1931	CB	GLU	A	375	-6.908	92.745	58.398	1.00	25.81	A	C
ATOM	1932	CG	GLU	A	375	-7.552	93.858	57.593	1.00	30.24	A	C
ATOM	1933	CD	GLU	A	375	-7.814	93.459	56.151	1.00	30.04	A	C
ATOM	1934	OE1	GLU	A	375	-8.843	92.800	55.883	1.00	33.09	A	O
ATOM	1935	OE2	GLU	A	375	-6.984	93.796	55.289	1.00	29.56	A	O
ATOM	1936	C	GLU	A	375	-6.143	91.864	60.612	1.00	25.25	A	C
ATOM	1937	O	GLU	A	375	-6.910	91.011	61.063	1.00	27.99	A	O
ATOM	1938	N	VAL	A	376	-4.820	91.785	60.727	1.00	22.91	A	N
ATOM	1939	CA	VAL	A	376	-4.175	90.687	61.439	1.00	21.50	A	C
ATOM	1940	CB	VAL	A	376	-2.643	90.662	61.187	1.00	21.90	A	C
ATOM	1941	CG1	VAL	A	376	-1.976	89.654	62.125	1.00	19.51	A	C
ATOM	1942	CG2	VAL	A	376	-2.355	90.313	59.729	1.00	22.63	A	C
ATOM	1943	C	VAL	A	376	-4.405	90.862	62.944	1.00	21.43	A	C
ATOM	1944	O	VAL	A	376	-4.725	89.906	63.653	1.00	19.70	A	O
ATOM	1945	N	LEU	A	377	-4.241	92.090	63.422	1.00	19.23	A	N
ATOM	1946	CA	LEU	A	377	-4.426	92.375	64.837	1.00	22.49	A	C
ATOM	1947	CB	LEU	A	377	-4.002	93.815	65.142	1.00	22.58	A	C
ATOM	1948	CG	LEU	A	377	-2.498	94.047	64.962	1.00	22.54	A	C
ATOM	1949	CD1	LEU	A	377	-2.172	95.525	64.951	1.00	22.51	A	C
ATOM	1950	CD2	LEU	A	377	-1.753	93.341	66.092	1.00	22.08	A	C
ATOM	1951	C	LEU	A	377	-5.869	92.143	65.269	1.00	25.05	A	C
ATOM	1952	O	LEU	A	377	-6.141	91.905	66.443	1.00	26.04	A	O
ATOM	1953	N	GLU	A	378	-6.787	92.177	64.308	1.00	24.26	A	N
ATOM	1954	CA	GLU	A	378	-8.193	91.983	64.611	1.00	25.18	A	C
ATOM	1955	CB	GLU	A	378	-9.032	93.046	63.890	1.00	27.95	A	C
ATOM	1956	CG	GLU	A	378	-8.848	94.444	64.452	1.00	31.63	A	C
ATOM	1957	CD	GLU	A	378	-9.693	95.484	63.743	1.00	33.54	A	C
ATOM	1958	OE1	GLU	A	378	-9.894	96.568	64.334	1.00	35.00	A	O
ATOM	1959	OE2	GLU	A	378	-10.147	95.220	62.605	1.00	31.59	A	O
ATOM	1960	C	GLU	A	378	-8.713	90.597	64.251	1.00	24.15	A	C
ATOM	1961	O	GLU	A	378	-9.883	90.301	64.473	1.00	21.88	A	O

ATOM	1962	N	HIS	A	379	-7.860	89.742	63.702	1.00	22.41	A	N
ATOM	1963	CA	HIS	A	379	-8.322	88.410	63.337	1.00	22.38	A	C
ATOM	1964	CB	HIS	A	379	-7.200	87.624	62.665	1.00	18.92	A	C
ATOM	1965	CG	HIS	A	379	-7.650	86.333	62.050	1.00	16.62	A	C
ATOM	1966	CD2	HIS	A	379	-7.936	86.009	60.767	1.00	15.24	A	C
ATOM	1967	ND1	HIS	A	379	-7.834	85.181	62.786	1.00	15.11	A	N
ATOM	1968	CE1	HIS	A	379	-8.208	84.202	61.982	1.00	16.55	A	C
ATOM	1969	NE2	HIS	A	379	-8.278	84.678	60.751	1.00	17.07	A	N
ATOM	1970	C	HIS	A	379	-8.818	87.695	64.595	1.00	22.89	A	C
ATOM	1971	O	HIS	A	379	-8.211	87.802	65.659	1.00	24.73	A	O
ATOM	1972	N	PRO	A	380	-9.948	86.978	64.489	1.00	22.77	A	N
ATOM	1973	CD	PRO	A	380	-10.751	86.800	63.266	1.00	22.48	A	C
ATOM	1974	CA	PRO	A	380	-10.544	86.247	65.614	1.00	22.16	A	C
ATOM	1975	CB	PRO	A	380	-11.777	85.580	64.984	1.00	22.20	A	C
ATOM	1976	CG	PRO	A	380	-11.422	85.482	63.529	1.00	24.64	A	C
ATOM	1977	C	PRO	A	380	-9.633	85.256	66.351	1.00	21.00	A	C
ATOM	1978	O	PRO	A	380	-9.762	85.078	67.563	1.00	19.68	A	O
ATOM	1979	N	TRP	A	381	-8.722	84.613	65.627	1.00	19.43	A	N
ATOM	1980	CA	TRP	A	381	-7.801	83.666	66.246	1.00	18.47	A	C
ATOM	1981	CB	TRP	A	381	-7.098	82.827	65.172	1.00	17.30	A	C
ATOM	1982	CG	TRP	A	381	-6.164	81.805	65.737	1.00	19.05	A	C
ATOM	1983	CD2	TRP	A	381	-4.733	81.895	65.800	1.00	18.83	A	C
ATOM	1984	CE2	TRP	A	381	-4.270	80.732	66.456	1.00	19.95	A	C
ATOM	1985	CE3	TRP	A	381	-3.800	82.846	65.366	1.00	19.48	A	C
ATOM	1986	CD1	TRP	A	381	-6.499	80.628	66.336	1.00	18.42	A	C
ATOM	1987	NE1	TRP	A	381	-5.368	79.975	66.771	1.00	18.35	A	N
ATOM	1988	CZ2	TRP	A	381	-2.907	80.493	66.690	1.00	18.02	A	C
ATOM	1989	CZ3	TRP	A	381	-2.440	82.609	65.597	1.00	19.48	A	C
ATOM	1990	CH2	TRP	A	381	-2.011	81.439	66.254	1.00	19.82	A	C
ATOM	1991	C	TRP	A	381	-6.764	84.430	67.088	1.00	18.12	A	C
ATOM	1992	O	TRP	A	381	-6.385	83.991	68.176	1.00	18.12	A	O
ATOM	1993	N	ILE	A	382	-6.324	85.579	66.587	1.00	18.20	A	N
ATOM	1994	CA	ILE	A	382	-5.347	86.410	67.296	1.00	19.68	A	C
ATOM	1995	CB	ILE	A	382	-4.875	87.569	66.394	1.00	17.49	A	C
ATOM	1996	CG2	ILE	A	382	-4.118	88.599	67.213	1.00	20.81	A	C
ATOM	1997	CG1	ILE	A	382	-4.020	87.021	65.243	1.00	18.99	A	C
ATOM	1998	CD1	ILE	A	382	-2.653	86.493	65.655	1.00	19.59	A	C
ATOM	1999	C	ILE	A	382	-5.932	86.997	68.592	1.00	22.60	A	C
ATOM	2000	O	ILE	A	382	-5.271	87.019	69.642	1.00	21.36	A	O
ATOM	2001	N	THR	A	383	-7.174	87.469	68.504	1.00	21.35	A	N
ATOM	2002	CA	THR	A	383	-7.886	88.068	69.632	1.00	22.03	A	C
ATOM	2003	CB	THR	A	383	-9.213	88.734	69.143	1.00	24.29	A	C
ATOM	2004	OG1	THR	A	383	-8.912	89.957	68.457	1.00	28.50	A	O
ATOM	2005	CG2	THR	A	383	-10.140	89.028	70.312	1.00	28.56	A	C
ATOM	2006	C	THR	A	383	-8.225	87.040	70.713	1.00	21.21	A	C
ATOM	2007	O	THR	A	383	-8.139	87.316	71.904	1.00	19.20	A	O
ATOM	2008	N	ALA	A	384	-8.622	85.849	70.285	1.00	21.12	A	N
ATOM	2009	CA	ALA	A	384	-8.986	84.788	71.217	1.00	19.34	A	C
ATOM	2010	CB	ALA	A	384	-9.661	83.649	70.448	1.00	16.55	A	C
ATOM	2011	C	ALA	A	384	-7.822	84.231	72.049	1.00	21.30	A	C
ATOM	2012	O	ALA	A	384	-7.980	83.995	73.259	1.00	22.43	A	O
ATOM	2013	N	ASN	A	385	-6.661	84.040	71.416	1.00	20.05	A	N
ATOM	2014	CA	ASN	A	385	-5.503	83.449	72.091	1.00	22.78	A	C
ATOM	2015	CB	ASN	A	385	-4.883	82.377	71.195	1.00	20.49	A	C
ATOM	2016	CG	ASN	A	385	-5.871	81.286	70.817	1.00	21.65	A	C
ATOM	2017	OD1	ASN	A	385	-6.380	80.569	71.674	1.00	21.14	A	O
ATOM	2018	ND2	ASN	A	385	-6.148	81.160	69.525	1.00	19.14	A	N
ATOM	2019	C	ASN	A	385	-4.385	84.356	72.593	1.00	25.16	A	C
ATOM	2020	O	ASN	A	385	-3.472	83.883	73.267	1.00	27.83	A	O
ATOM	2021	N	SER	A	386	-4.426	85.642	72.274	1.00	26.88	A	N
ATOM	2022	CA	SER	A	386	-3.375	86.536	72.739	1.00	29.74	A	C
ATOM	2023	CB	SER	A	386	-3.385	87.834	71.940	1.00	30.28	A	C
ATOM	2024	OG	SER	A	386	-2.391	88.717	72.419	1.00	33.08	A	O
ATOM	2025	C	SER	A	386	-3.559	86.851	74.218	1.00	32.93	A	C
ATOM	2026	O	SER	A	386	-4.677	87.088	74.676	1.00	32.42	A	O
ATOM	2027	N	SER	A	387	-2.461	86.844	74.967	1.00	34.64	A	N
ATOM	2028	CA	SER	A	387	-2.524	87.144	76.393	1.00	37.99	A	C
ATOM	2029	CB	SER	A	387	-1.376	86.454	77.141	1.00	38.92	A	C
ATOM	2030	OG	SER	A	387	-0.112	86.876	76.662	1.00	37.92	A	O
ATOM	2031	C	SER	A	387	-2.451	88.652	76.599	1.00	39.48	A	C
ATOM	2032	O	SER	A	387	-2.459	89.135	77.728	1.00	40.65	A	O
ATOM	2033	N	LYS	A	388	-2.387	89.383	75.489	1.00	41.58	A	N

ATOM	2034	CA	LYS	A	388	-2.320	90.844	75.487	1.00	43.93	A	C
ATOM	2035	CB	LYS	A	388	-3.340	91.441	76.466	1.00	43.62	A	C
ATOM	2036	CG	LYS	A	388	-4.758	90.887	76.316	1.00	43.37	A	C
ATOM	2037	CD	LYS	A	388	-5.787	91.767	77.016	1.00	43.10	A	C
ATOM	2038	CE	LYS	A	388	-6.533	92.633	75.989	1.00	43.79	A	C
ATOM	2039	NZ	LYS	A	388	-5.609	93.345	75.045	1.00	42.84	A	N
ATOM	2040	C	LYS	A	388	-0.918	91.354	75.822	1.00	45.61	A	C
ATOM	2041	O	LYS	A	388	-0.649	91.581	77.023	1.00	46.51	A	O
ATOM	2042	OXT	LYS	A	388	-0.100	91.503	74.881	1.00	46.24	A	O
TER	2043		LYS	A	388							
ATOM	2044	CB	GLN	B	126	10.213	7.246	17.228	1.00	52.35	B	C
ATOM	2045	CG	GLN	B	126	11.292	7.078	16.169	1.00	53.31	B	C
ATOM	2046	CD	GLN	B	126	12.534	6.382	16.706	1.00	54.51	B	C
ATOM	2047	OE1	GLN	B	126	13.488	6.131	15.966	1.00	55.84	B	O
ATOM	2048	NE2	GLN	B	126	12.526	6.065	17.999	1.00	53.41	B	N
ATOM	2049	C	GLN	B	126	8.987	9.170	16.193	1.00	50.24	B	C
ATOM	2050	O	GLN	B	126	8.930	9.438	14.994	1.00	50.75	B	O
ATOM	2051	N	GLN	B	126	8.388	6.816	15.605	1.00	51.32	B	N
ATOM	2052	CA	GLN	B	126	8.864	7.730	16.685	1.00	51.36	B	C
ATOM	2053	N	TRP	B	127	9.168	10.087	17.137	1.00	48.65	B	N
ATOM	2054	CA	TRP	B	127	9.279	11.516	16.855	1.00	45.05	B	C
ATOM	2055	CB	TRP	B	127	9.752	12.240	18.112	1.00	45.82	B	C
ATOM	2056	CG	TRP	B	127	8.716	12.256	19.197	1.00	48.91	B	C
ATOM	2057	CD2	TRP	B	127	7.325	12.583	19.052	1.00	49.46	B	C
ATOM	2058	CE2	TRP	B	127	6.741	12.502	20.336	1.00	50.15	B	C
ATOM	2059	CE3	TRP	B	127	6.517	12.937	17.962	1.00	50.60	B	C
ATOM	2060	CD1	TRP	B	127	8.911	11.997	20.523	1.00	49.18	B	C
ATOM	2061	NE1	TRP	B	127	7.730	12.143	21.214	1.00	50.57	B	N
ATOM	2062	CZ2	TRP	B	127	5.384	12.764	20.563	1.00	51.76	B	C
ATOM	2063	CZ3	TRP	B	127	5.163	13.197	18.186	1.00	51.62	B	C
ATOM	2064	CH2	TRP	B	127	4.613	13.108	19.479	1.00	51.32	B	C
ATOM	2065	C	TRP	B	127	10.131	11.952	15.671	1.00	42.62	B	C
ATOM	2066	O	TRP	B	127	11.322	11.660	15.593	1.00	42.25	B	O
ATOM	2067	N	ALA	B	128	9.488	12.664	14.749	1.00	39.75	B	N
ATOM	2068	CA	ALA	B	128	10.141	13.206	13.564	1.00	36.83	B	C
ATOM	2069	CB	ALA	B	128	9.858	12.342	12.342	1.00	37.27	B	C
ATOM	2070	C	ALA	B	128	9.533	14.584	13.386	1.00	33.84	B	C
ATOM	2071	O	ALA	B	128	8.469	14.862	13.929	1.00	33.46	B	O
ATOM	2072	N	LEU	B	129	10.201	15.443	12.630	1.00	32.37	B	N
ATOM	2073	CA	LEU	B	129	9.718	16.798	12.419	1.00	32.04	B	C
ATOM	2074	CB	LEU	B	129	10.708	17.570	11.548	1.00	31.51	B	C
ATOM	2075	CG	LEU	B	129	10.548	19.091	11.537	1.00	33.77	B	C
ATOM	2076	CD1	LEU	B	129	10.560	19.625	12.968	1.00	33.40	B	C
ATOM	2077	CD2	LEU	B	129	11.673	19.708	10.731	1.00	32.31	B	C
ATOM	2078	C	LEU	B	129	8.321	16.854	11.796	1.00	31.97	B	C
ATOM	2079	O	LEU	B	129	7.479	17.645	12.226	1.00	31.99	B	O
ATOM	2080	N	ALA	B	130	8.082	16.007	10.797	1.00	31.30	B	N
ATOM	2081	CA	ALA	B	130	6.803	15.951	10.091	1.00	31.88	B	C
ATOM	2082	CB	ALA	B	130	6.866	14.898	8.983	1.00	31.86	B	C
ATOM	2083	C	ALA	B	130	5.609	15.677	10.995	1.00	31.10	B	C
ATOM	2084	O	ALA	B	130	4.465	15.794	10.568	1.00	32.53	B	O
ATOM	2085	N	ASP	B	131	5.871	15.312	12.243	1.00	30.37	B	N
ATOM	2086	CA	ASP	B	131	4.800	15.038	13.193	1.00	30.59	B	C
ATOM	2087	CB	ASP	B	131	5.329	14.156	14.328	1.00	32.68	B	C
ATOM	2088	CG	ASP	B	131	5.607	12.727	13.884	1.00	36.29	B	C
ATOM	2089	OD1	ASP	B	131	6.370	12.025	14.582	1.00	36.01	B	O
ATOM	2090	OD2	ASP	B	131	5.053	12.302	12.847	1.00	36.71	B	O
ATOM	2091	C	ASP	B	131	4.197	16.309	13.796	1.00	29.73	B	C
ATOM	2092	O	ASP	B	131	3.185	16.242	14.492	1.00	30.13	B	O
ATOM	2093	N	PHE	B	132	4.800	17.462	13.512	1.00	28.26	B	N
ATOM	2094	CA	PHE	B	132	4.344	18.725	14.092	1.00	25.47	B	C
ATOM	2095	CB	PHE	B	132	5.417	19.272	15.039	1.00	25.53	B	C
ATOM	2096	CG	PHE	B	132	5.944	18.268	16.020	1.00	25.89	B	C
ATOM	2097	CD1	PHE	B	132	5.301	18.056	17.234	1.00	27.37	B	C
ATOM	2098	CD2	PHE	B	132	7.087	17.536	15.732	1.00	26.04	B	C
ATOM	2099	CE1	PHE	B	132	5.791	17.130	18.144	1.00	28.04	B	C
ATOM	2100	CE2	PHE	B	132	7.584	16.608	16.633	1.00	26.31	B	C
ATOM	2101	CZ	PHE	B	132	6.937	16.403	17.839	1.00	27.54	B	C
ATOM	2102	C	PHE	B	132	4.020	19.855	13.127	1.00	25.28	B	C
ATOM	2103	O	PHE	B	132	4.581	19.946	12.039	1.00	23.06	B	O
ATOM	2104	N	GLU	B	133	3.113	20.724	13.567	1.00	24.47	B	N
ATOM	2105	CA	GLU	B	133	2.751	21.929	12.835	1.00	24.02	B	C

ATOM	2106	CB	GLU	B	133	1.234	22.125	12.779	1.00	26.65	B	C
ATOM	2107	CG	GLU	B	133	0.586	21.444	11.597	1.00	32.34	B	C
ATOM	2108	CD	GLU	B	133	-0.806	21.962	11.312	1.00	36.67	B	C
ATOM	2109	OE1	GLU	B	133	-1.355	21.615	10.245	1.00	38.29	B	O
ATOM	2110	OE2	GLU	B	133	-1.348	22.715	12.151	1.00	38.65	B	O
ATOM	2111	C	GLU	B	133	3.387	23.029	13.678	1.00	22.07	B	C
ATOM	2112	O	GLU	B	133	3.123	23.122	14.873	1.00	19.84	B	O
ATOM	2113	N	ILE	B	134	4.228	23.842	13.051	1.00	22.05	B	N
ATOM	2114	CA	ILE	B	134	4.957	24.924	13.718	1.00	20.74	B	C
ATOM	2115	CB	ILE	B	134	6.356	25.077	13.065	1.00	22.02	B	C
ATOM	2116	CG2	ILE	B	134	7.127	26.232	13.692	1.00	19.99	B	C
ATOM	2117	CG1	ILE	B	134	7.121	23.758	13.219	1.00	22.38	B	C
ATOM	2118	CD1	ILE	B	134	8.451	23.728	12.488	1.00	26.58	B	C
ATOM	2119	C	ILE	B	134	4.226	26.259	13.661	1.00	20.52	B	C
ATOM	2120	O	ILE	B	134	3.688	26.621	12.618	1.00	21.50	B	O
ATOM	2121	N	GLY	B	135	4.222	26.989	14.778	1.00	19.55	B	N
ATOM	2122	CA	GLY	B	135	3.547	28.282	14.846	1.00	19.33	B	C
ATOM	2123	C	GLY	B	135	4.485	29.464	15.035	1.00	19.91	B	C
ATOM	2124	O	GLY	B	135	5.614	29.435	14.563	1.00	18.49	B	O
ATOM	2125	N	ARG	B	136	4.034	30.499	15.739	1.00	21.61	B	N
ATOM	2126	CA	ARG	B	136	4.857	31.695	15.970	1.00	23.20	B	C
ATOM	2127	CB	ARG	B	136	4.014	32.824	16.570	1.00	24.31	B	C
ATOM	2128	CG	ARG	B	136	3.656	32.619	18.042	1.00	27.58	B	C
ATOM	2129	CD	ARG	B	136	2.652	33.652	18.548	1.00	28.19	B	C
ATOM	2130	NE	ARG	B	136	2.162	33.295	19.877	1.00	29.58	B	N
ATOM	2131	CZ	ARG	B	136	2.671	33.747	21.023	1.00	30.89	B	C
ATOM	2132	NH1	ARG	B	136	3.692	34.598	21.016	1.00	28.09	B	N
ATOM	2133	NH2	ARG	B	136	2.167	33.326	22.182	1.00	29.68	B	N
ATOM	2134	C	ARG	B	136	6.049	31.460	16.895	1.00	22.61	B	C
ATOM	2135	O	ARG	B	136	6.019	30.597	17.762	1.00	22.20	B	O
ATOM	2136	N	PRO	B	137	7.126	32.231	16.709	1.00	24.01	B	N
ATOM	2137	CD	PRO	B	137	7.425	33.170	15.611	1.00	24.72	B	C
ATOM	2138	CA	PRO	B	137	8.287	32.047	17.581	1.00	23.55	B	C
ATOM	2139	CB	PRO	B	137	9.393	32.798	16.840	1.00	26.09	B	C
ATOM	2140	CG	PRO	B	137	8.637	33.905	16.144	1.00	26.11	B	C
ATOM	2141	C	PRO	B	137	7.976	32.627	18.965	1.00	23.34	B	C
ATOM	2142	O	PRO	B	137	7.350	33.682	19.088	1.00	22.43	B	O
ATOM	2143	N	LEU	B	138	8.390	31.909	20.000	1.00	22.77	B	N
ATOM	2144	CA	LEU	B	138	8.153	32.316	21.383	1.00	25.08	B	C
ATOM	2145	CB	LEU	B	138	7.909	31.077	22.247	1.00	23.93	B	C
ATOM	2146	CG	LEU	B	138	6.501	30.564	22.574	1.00	25.09	B	C
ATOM	2147	CD1	LEU	B	138	5.475	30.991	21.532	1.00	21.71	B	C
ATOM	2148	CD2	LEU	B	138	6.575	29.054	22.715	1.00	22.09	B	C
ATOM	2149	C	LEU	B	138	9.361	33.076	21.908	1.00	27.37	B	C
ATOM	2150	O	LEU	B	138	9.253	33.860	22.842	1.00	29.02	B	O
ATOM	2151	N	GLY	B	139	10.511	32.831	21.292	1.00	30.52	B	N
ATOM	2152	CA	GLY	B	139	11.736	33.487	21.701	1.00	33.40	B	C
ATOM	2153	C	GLY	B	139	12.887	33.087	20.796	1.00	36.61	B	C
ATOM	2154	O	GLY	B	139	12.829	32.049	20.125	1.00	34.75	B	O
ATOM	2155	N	ALA	B	140	13.931	33.917	20.775	1.00	38.80	B	N
ATOM	2156	CA	ALA	B	140	15.151	33.669	19.952	1.00	41.45	B	C
ATOM	2157	CB	ALA	B	140	15.197	34.703	18.839	1.00	41.02	B	C
ATOM	2158	C	ALA	B	140	16.348	33.742	20.833	1.00	42.68	B	C
ATOM	2159	O	ALA	B	140	16.614	34.774	21.443	1.00	44.14	B	O
ATOM	2160	N	ALA	B	141	17.091	32.640	20.905	1.00	43.65	B	N
ATOM	2161	CA	ALA	B	141	18.295	32.567	21.728	1.00	43.81	B	C
ATOM	2162	CB	ALA	B	141	18.233	31.342	22.638	1.00	45.73	B	C
ATOM	2163	C	ALA	B	141	19.553	32.515	20.872	1.00	43.24	B	C
ATOM	2164	O	ALA	B	141	19.501	32.748	19.669	1.00	41.60	B	O
ATOM	2165	N	ALA	B	142	20.682	32.203	21.502	1.00	43.17	B	N
ATOM	2166	CA	ALA	B	142	21.956	32.136	20.794	1.00	43.89	B	C
ATOM	2167	CB	ALA	B	142	23.107	32.336	21.774	1.00	43.83	B	C
ATOM	2168	C	ALA	B	142	22.146	30.826	20.032	1.00	44.32	B	C
ATOM	2169	O	ALA	B	142	22.701	30.817	18.932	1.00	45.04	B	O
ATOM	2170	N	PHE	B	143	21.682	29.723	20.612	1.00	43.15	B	N
ATOM	2171	CA	PHE	B	143	21.829	28.421	19.973	1.00	41.85	B	C
ATOM	2172	CB	PHE	B	143	22.102	27.350	21.025	1.00	43.72	B	C
ATOM	2173	CG	PHE	B	143	23.254	27.671	21.931	1.00	47.41	B	C
ATOM	2174	CD1	PHE	B	143	23.098	28.563	22.986	1.00	48.28	B	C
ATOM	2175	CD2	PHE	B	143	24.496	27.079	21.733	1.00	47.70	B	C
ATOM	2176	CE1	PHE	B	143	24.162	28.858	23.832	1.00	49.52	B	C
ATOM	2177	CE2	PHE	B	143	25.564	27.368	22.572	1.00	48.56	B	C

	ATOM	2178	CZ	PHE	B	143	25.398	28.259	23.624	1.00	48.11	B	C
	ATOM	2179	C	PHE	B	143	20.625	28.002	19.127	1.00	39.85	B	C
	ATOM	2180	O	PHE	B	143	20.673	26.972	18.453	1.00	37.97	B	O
	ATOM	2181	N	GLY	B	144	19.554	28.792	19.164	1.00	37.20	B	N
5	ATOM	2182	CA	GLY	B	144	18.374	28.461	18.386	1.00	35.94	B	C
	ATOM	2183	C	GLY	B	144	17.111	29.160	18.851	1.00	35.06	B	C
	ATOM	2184	O	GLY	B	144	17.172	30.161	19.565	1.00	34.22	B	O
	ATOM	2185	N	ASN	B	145	15.959	28.628	18.449	1.00	33.13	B	N
	ATOM	2186	CA	ASN	B	145	14.682	29.228	18.826	1.00	31.01	B	C
10	ATOM	2187	CB	ASN	B	145	14.082	29.980	17.639	1.00	33.45	B	C
	ATOM	2188	CG	ASN	B	145	15.124	30.694	16.824	1.00	36.83	B	C
	ATOM	2189	OD1	ASN	B	145	15.849	30.072	16.051	1.00	39.85	B	O
	ATOM	2190	ND2	ASN	B	145	15.220	32.010	16.999	1.00	39.53	B	N
	ATOM	2191	C	ASN	B	145	13.654	28.225	19.318	1.00	27.19	B	C
15	ATOM	2192	O	ASN	B	145	13.751	27.026	19.053	1.00	26.12	B	O
	ATOM	2193	N	VAL	B	146	12.663	28.745	20.030	1.00	23.46	B	N
	ATOM	2194	CA	VAL	B	146	11.568	27.951	20.568	1.00	21.53	B	C
	ATOM	2195	CB	VAL	B	146	11.382	28.182	22.086	1.00	21.61	B	C
	ATOM	2196	CG1	VAL	B	146	10.329	27.242	22.623	1.00	22.87	B	C
20	ATOM	2197	CG2	VAL	B	146	12.688	27.990	22.807	1.00	26.97	B	C
	ATOM	2198	C	VAL	B	146	10.307	28.447	19.865	1.00	20.89	B	C
	ATOM	2199	O	VAL	B	146	10.087	29.657	19.774	1.00	18.61	B	O
	ATOM	2200	N	TYR	B	147	9.489	27.518	19.379	1.00	18.85	B	N
	ATOM	2201	CA	TYR	B	147	8.254	27.866	18.688	1.00	18.39	B	C
25	ATOM	2202	CB	TYR	B	147	8.273	27.362	17.239	1.00	17.65	B	C
	ATOM	2203	CG	TYR	B	147	9.420	27.846	16.400	1.00	17.80	B	C
	ATOM	2204	CD1	TYR	B	147	10.654	27.186	16.409	1.00	19.71	B	C
	ATOM	2205	CE1	TYR	B	147	11.726	27.653	15.629	1.00	20.17	B	C
	ATOM	2206	CD2	TYR	B	147	9.281	28.976	15.598	1.00	17.79	B	C
30	ATOM	2207	CE2	TYR	B	147	10.336	29.447	14.823	1.00	16.88	B	C
	ATOM	2208	CZ	TYR	B	147	11.550	28.791	14.840	1.00	17.99	B	C
	ATOM	2209	OH	TYR	B	147	12.582	29.292	14.078	1.00	21.66	B	O
	ATOM	2210	C	TYR	B	147	7.050	27.218	19.349	1.00	17.88	B	C
	ATOM	2211	O	TYR	B	147	7.180	26.186	20.000	1.00	17.17	B	O
35	ATOM	2212	N	LEU	B	148	5.880	27.829	19.188	1.00	17.80	B	N
	ATOM	2213	CA	LEU	B	148	4.661	27.208	19.688	1.00	18.36	B	C
	ATOM	2214	CB	LEU	B	148	3.478	28.172	19.616	1.00	22.50	B	C
	ATOM	2215	CG	LEU	B	148	2.102	27.595	19.990	1.00	23.22	B	C
	ATOM	2216	CD1	LEU	B	148	2.017	27.353	21.494	1.00	24.62	B	C
40	ATOM	2217	CD2	LEU	B	148	1.016	28.563	19.559	1.00	25.28	B	C
	ATOM	2218	C	LEU	B	148	4.475	26.107	18.641	1.00	19.19	B	C
	ATOM	2219	O	LEU	B	148	4.881	26.289	17.476	1.00	18.41	B	O
	ATOM	2220	N	ALA	B	149	3.941	24.959	19.034	1.00	18.74	B	N
	ATOM	2221	CA	ALA	B	149	3.734	23.900	18.063	1.00	21.02	B	C
45	ATOM	2222	CB	ALA	B	149	5.005	23.057	17.907	1.00	22.54	B	C
	ATOM	2223	C	ALA	B	149	2.560	23.018	18.429	1.00	22.53	B	C
	ATOM	2224	O	ALA	B	149	2.109	23.002	19.573	1.00	22.04	B	O
	ATOM	2225	N	ARG	B	150	2.060	22.286	17.444	1.00	23.48	B	N
	ATOM	2226	CA	ARG	B	150	0.932	21.402	17.667	1.00	26.45	B	C
50	ATOM	2227	CB	ARG	B	150	-0.349	22.081	17.176	1.00	27.56	B	C
	ATOM	2228	CG	ARG	B	150	-1.626	21.299	17.419	1.00	31.39	B	C
	ATOM	2229	CD	ARG	B	150	-2.817	22.249	17.534	1.00	33.89	B	C
	ATOM	2230	NE	ARG	B	150	-2.772	23.313	16.534	1.00	37.25	B	N
	ATOM	2231	CZ	ARG	B	150	-3.463	24.447	16.616	1.00	38.06	B	C
55	ATOM	2232	NH1	ARG	B	150	-4.258	24.669	17.655	1.00	39.33	B	N
	ATOM	2233	NH2	ARG	B	150	-3.350	25.367	15.664	1.00	37.88	B	N
	ATOM	2234	C	ARG	B	150	1.157	20.075	16.957	1.00	27.39	B	C
	ATOM	2235	O	ARG	B	150	1.540	20.044	15.785	1.00	26.15	B	O
	ATOM	2236	N	GLU	B	151	0.953	18.978	17.680	1.00	28.95	B	N
60	ATOM	2237	CA	GLU	B	151	1.130	17.657	17.092	1.00	33.02	B	C
	ATOM	2238	CB	GLU	B	151	1.153	16.597	18.186	1.00	34.21	B	C
	ATOM	2239	CG	GLU	B	151	1.901	15.344	17.795	1.00	39.51	B	C
	ATOM	2240	CD	GLU	B	151	1.687	14.213	18.781	1.00	43.41	B	C
	ATOM	2241	OE1	GLU	B	151	1.948	14.412	19.991	1.00	44.45	B	O
65	ATOM	2242	OE2	GLU	B	151	1.257	13.122	18.342	1.00	46.66	B	O
	ATOM	2243	C	GLU	B	151	-0.031	17.402	16.123	1.00	33.90	B	C
	ATOM	2244	O	GLU	B	151	-1.187	17.611	16.470	1.00	31.69	B	O
	ATOM	2245	N	LYS	B	152	0.281	16.958	14.911	1.00	36.17	B	N
	ATOM	2246	CA	LYS	B	152	-0.747	16.718	13.901	1.00	39.16	B	C
70	ATOM	2247	CB	LYS	B	152	-0.103	16.292	12.579	1.00	38.11	B	C
	ATOM	2248	CG	LYS	B	152	0.598	17.422	11.855	1.00	37.99	B	C
	ATOM	2249	CD	LYS	B	152	1.208	16.952	10.554	1.00	39.08	B	C

	ATOM	2250	CE	LYS	B	152	1.924	18.091	9.855	1.00	40.02	B C
	ATOM	2251	NZ	LYS	B	152	2.654	17.635	8.642	1.00	41.02	B N
	ATOM	2252	C	LYS	B	152	-1.845	15.725	14.270	1.00	41.64	B C
	ATOM	2253	O	LYS	B	152	-3.033	16.047	14.171	1.00	41.11	B O
5	ATOM	2254	N	GLN	B	153	-1.459	14.523	14.688	1.00	44.21	B N
	ATOM	2255	CA	GLN	B	153	-2.445	13.505	15.040	1.00	46.53	B C
	ATOM	2256	CB	GLN	B	153	-1.756	12.244	15.553	1.00	48.92	B C
	ATOM	2257	CG	GLN	B	153	-2.672	11.035	15.561	1.00	53.13	B C
	ATOM	2258	CD	GLN	B	153	-3.378	10.842	14.226	1.00	55.60	B C
10	ATOM	2259	OE1	GLN	B	153	-2.735	10.731	13.177	1.00	56.44	B O
	ATOM	2260	NE2	GLN	B	153	-4.708	10.807	14.260	1.00	55.73	B N
	ATOM	2261	C	GLN	B	153	-3.427	14.022	16.082	1.00	46.20	B C
	ATOM	2262	O	GLN	B	153	-4.626	14.116	15.825	1.00	47.04	B O
	ATOM	2263	N	SER	B	154	-2.926	14.344	17.265	1.00	46.37	B N
15	ATOM	2264	CA	SER	B	154	-3.791	14.879	18.305	1.00	46.19	B C
	ATOM	2265	CB	SER	B	154	-3.206	14.591	19.690	1.00	45.90	B C
	ATOM	2266	OG	SER	B	154	-1.871	15.057	19.798	1.00	45.56	B O
	ATOM	2267	C	SER	B	154	-3.847	16.379	18.046	1.00	46.16	B C
	ATOM	2268	O	SER	B	154	-3.415	16.846	16.995	1.00	47.31	B O
20	ATOM	2269	N	LYS	B	155	-4.387	17.139	18.981	1.00	45.67	B N
	ATOM	2270	CA	LYS	B	155	-4.450	18.582	18.806	1.00	45.70	B C
	ATOM	2271	CB	LYS	B	155	-5.916	19.031	18.799	1.00	48.89	B C
	ATOM	2272	CG	LYS	B	155	-6.128	20.540	18.761	1.00	52.40	B C
	ATOM	2273	CD	LYS	B	155	-6.349	21.108	20.159	1.00	53.23	B C
25	ATOM	2274	CE	LYS	B	155	-6.084	22.601	20.182	1.00	54.16	B C
	ATOM	2275	NZ	LYS	B	155	-4.697	22.904	19.726	1.00	53.54	B N
	ATOM	2276	C	LYS	B	155	-3.677	19.222	19.959	1.00	42.90	B C
	ATOM	2277	O	LYS	B	155	-3.770	20.423	20.207	1.00	43.52	B O
	ATOM	2278	N	PHE	B	156	-2.892	18.397	20.644	1.00	39.07	B N
30	ATOM	2279	CA	PHE	B	156	-2.108	18.824	21.796	1.00	35.93	B C
	ATOM	2280	CB	PHE	B	156	-1.375	17.615	22.377	1.00	37.42	B C
	ATOM	2281	CG	PHE	B	156	-0.841	17.834	23.761	1.00	39.54	B C
	ATOM	2282	CD1	PHE	B	156	-1.699	18.157	24.806	1.00	39.40	B C
	ATOM	2283	CD2	PHE	B	156	0.521	17.705	24.024	1.00	40.10	B C
35	ATOM	2284	CE1	PHE	B	156	-1.209	18.351	26.099	1.00	40.25	B C
	ATOM	2285	CE2	PHE	B	156	1.024	17.897	25.316	1.00	40.40	B C
	ATOM	2286	CZ	PHE	B	156	0.156	18.220	26.354	1.00	40.47	B C
	ATOM	2287	C	PHE	B	156	-1.111	19.943	21.487	1.00	32.41	B C
	ATOM	2288	O	PHE	B	156	-0.328	19.846	20.544	1.00	31.99	B O
40	ATOM	2289	N	ILE	B	157	-1.153	20.999	22.294	1.00	28.30	B N
	ATOM	2290	CA	ILE	B	157	-0.270	22.153	22.146	1.00	27.01	B C
	ATOM	2291	CB	ILE	B	157	-0.933	23.445	22.684	1.00	28.09	B C
	ATOM	2292	CG2	ILE	B	157	0.042	24.608	22.590	1.00	29.72	B C
	ATOM	2293	CG1	ILE	B	157	-2.212	23.754	21.899	1.00	29.62	B C
45	ATOM	2294	CD1	ILE	B	157	-1.977	24.215	20.480	1.00	32.78	B C
	ATOM	2295	C	ILE	B	157	1.016	21.934	22.936	1.00	24.58	B C
	ATOM	2296	O	ILE	B	157	0.990	21.436	24.060	1.00	23.83	B O
	ATOM	2297	N	LEU	B	158	2.141	22.320	22.353	1.00	23.27	B N
	ATOM	2298	CA	LEU	B	158	3.426	22.158	23.020	1.00	22.00	B C
50	ATOM	2299	CB	LEU	B	158	3.933	20.721	22.832	1.00	22.79	B C
	ATOM	2300	CG	LEU	B	158	3.978	20.154	21.407	1.00	26.19	B C
	ATOM	2301	CD1	LEU	B	158	5.220	20.663	20.676	1.00	25.77	B C
	ATOM	2302	CD2	LEU	B	158	3.991	18.632	21.463	1.00	24.53	B C
	ATOM	2303	C	LEU	B	158	4.438	23.165	22.491	1.00	20.27	B C
55	ATOM	2304	O	LEU	B	158	4.118	24.000	21.648	1.00	19.23	B O
	ATOM	2305	N	ALA	B	159	5.660	23.106	23.005	1.00	18.97	B N
	ATOM	2306	CA	ALA	B	159	6.695	24.016	22.552	1.00	16.46	B C
	ATOM	2307	CB	ALA	B	159	7.183	24.864	23.705	1.00	13.97	B C
60	ATOM	2308	C	ALA	B	159	7.826	23.189	21.967	1.00	16.51	B C
	ATOM	2309	O	ALA	B	159	8.214	22.169	22.536	1.00	16.62	B O
	ATOM	2310	N	LEU	B	160	8.330	23.614	20.813	1.00	16.01	B N
	ATOM	2311	CA	LEU	B	160	9.419	22.914	20.143	1.00	17.40	B C
	ATOM	2312	CB	LEU	B	160	9.002	22.524	18.712	1.00	19.02	B C
65	ATOM	2313	CG	LEU	B	160	10.016	21.678	17.928	1.00	20.39	B C
	ATOM	2314	CD1	LEU	B	160	10.062	20.269	18.520	1.00	21.64	B C
	ATOM	2315	CD2	LEU	B	160	9.628	21.606	16.459	1.00	21.97	B C
	ATOM	2316	C	LEU	B	160	10.648	23.821	20.092	1.00	16.96	B C
	ATOM	2317	O	LEU	B	160	10.582	24.930	19.581	1.00	17.75	B O
70	ATOM	2318	N	LYS	B	161	11.766	23.351	20.629	1.00	18.51	B N
	ATOM	2319	CA	LYS	B	161	13.002	24.136	20.624	1.00	19.34	B C
	ATOM	2320	CB	LYS	B	161	13.612	24.188	22.039	1.00	19.45	B C

ATOM	2321	CG	LYS	B	161	14.832	25.113	22.166	1.00	20.17	B	C
ATOM	2322	CD	LYS	B	161	15.129	25.442	23.625	1.00	20.81	B	C
ATOM	2323	CE	LYS	B	161	16.291	26.407	23.767	1.00	22.49	B	C
ATOM	2324	NZ	LYS	B	161	16.427	26.941	25.152	1.00	23.30	B	N
ATOM	2325	C	LYS	B	161	13.987	23.520	19.637	1.00	19.59	B	C
ATOM	2326	O	LYS	B	161	14.296	22.329	19.708	1.00	20.16	B	O
ATOM	2327	N	VAL	B	162	14.471	24.336	18.709	1.00	19.67	B	N
ATOM	2328	CA	VAL	B	162	15.402	23.867	17.688	1.00	21.10	B	C
ATOM	2329	CB	VAL	B	162	14.945	24.292	16.276	1.00	22.26	B	C
ATOM	2330	CG1	VAL	B	162	15.813	23.623	15.235	1.00	24.01	B	C
ATOM	2331	CG2	VAL	B	162	13.465	23.934	16.058	1.00	22.27	B	C
ATOM	2332	C	VAL	B	162	16.800	24.430	17.908	1.00	21.17	B	C
ATOM	2333	O	VAL	B	162	16.993	25.642	17.848	1.00	19.86	B	O
ATOM	2334	N	LEU	B	163	17.768	23.544	18.133	1.00	21.64	B	N
ATOM	2335	CA	LEU	B	163	19.157	23.950	18.369	1.00	20.49	B	C
ATOM	2336	CB	LEU	B	163	19.651	23.326	19.670	1.00	20.44	B	C
ATOM	2337	CG	LEU	B	163	18.813	23.620	20.912	1.00	22.02	B	C
ATOM	2338	CD1	LEU	B	163	19.087	22.573	21.978	1.00	22.74	B	C
ATOM	2339	CD2	LEU	B	163	19.121	25.026	21.417	1.00	22.92	B	C
ATOM	2340	C	LEU	B	163	20.094	23.542	17.234	1.00	21.79	B	C
ATOM	2341	O	LEU	B	163	19.998	22.422	16.707	1.00	22.08	B	O
ATOM	2342	N	PHE	B	164	21.008	24.441	16.861	1.00	22.17	B	N
ATOM	2343	CA	PHE	B	164	21.968	24.157	15.795	1.00	22.32	B	C
ATOM	2344	CB	PHE	B	164	22.261	25.419	14.985	1.00	23.92	B	C
ATOM	2345	CG	PHE	B	164	21.063	25.946	14.256	1.00	30.95	B	C
ATOM	2346	CD1	PHE	B	164	20.081	26.667	14.934	1.00	30.56	B	C
ATOM	2347	CD2	PHE	B	164	20.880	25.668	12.903	1.00	31.82	B	C
ATOM	2348	CE1	PHE	B	164	18.935	27.099	14.281	1.00	32.58	B	C
ATOM	2349	CE2	PHE	B	164	19.733	26.096	12.238	1.00	34.84	B	C
ATOM	2350	CZ	PHE	B	164	18.758	26.813	12.930	1.00	34.24	B	C
ATOM	2351	C	PHE	B	164	23.251	23.598	16.382	1.00	22.61	B	C
ATOM	2352	O	PHE	B	164	23.925	24.261	17.176	1.00	22.86	B	O
ATOM	2353	N	LYS	B	165	23.582	22.371	15.994	1.00	22.67	B	N
ATOM	2354	CA	LYS	B	165	24.777	21.711	16.511	1.00	22.73	B	C
ATOM	2355	CB	LYS	B	165	24.982	20.360	15.827	1.00	21.42	B	C
ATOM	2356	CG	LYS	B	165	24.153	19.240	16.419	1.00	21.02	B	C
ATOM	2357	CD	LYS	B	165	24.153	18.010	15.506	1.00	22.54	B	C
ATOM	2358	CE	LYS	B	165	23.243	16.926	16.062	1.00	22.64	B	C
ATOM	2359	NZ	LYS	B	165	23.231	15.701	15.230	1.00	21.04	B	N
ATOM	2360	C	LYS	B	165	26.051	22.533	16.388	1.00	23.20	B	C
ATOM	2361	O	LYS	B	165	26.865	22.548	17.312	1.00	21.71	B	O
ATOM	2362	N	ALA	B	166	26.215	23.219	15.261	1.00	22.64	B	N
ATOM	2363	CA	ALA	B	166	27.416	24.013	15.026	1.00	24.25	B	C
ATOM	2364	CB	ALA	B	166	27.384	24.629	13.613	1.00	24.20	B	C
ATOM	2365	C	ALA	B	166	27.636	25.098	16.072	1.00	24.80	B	C
ATOM	2366	O	ALA	B	166	28.772	25.333	16.491	1.00	24.79	B	O
ATOM	2367	N	GLN	B	167	26.563	25.758	16.495	1.00	25.16	B	N
ATOM	2368	CA	GLN	B	167	26.684	26.810	17.503	1.00	26.89	B	C
ATOM	2369	CB	GLN	B	167	25.411	27.660	17.545	1.00	29.97	B	C
ATOM	2370	CG	GLN	B	167	25.203	28.462	18.834	1.00	37.08	B	C
ATOM	2371	CD	GLN	B	167	26.215	29.587	19.035	1.00	42.68	B	C
ATOM	2372	OE1	GLN	B	167	27.425	29.351	19.185	1.00	43.86	B	O
ATOM	2373	NE2	GLN	B	167	25.719	30.824	19.042	1.00	43.02	B	N
ATOM	2374	C	GLN	B	167	26.950	26.193	18.866	1.00	26.35	B	C
ATOM	2375	O	GLN	B	167	27.707	26.739	19.672	1.00	24.45	B	O
ATOM	2376	N	LEU	B	168	26.334	25.041	19.111	1.00	25.56	B	N
ATOM	2377	CA	LEU	B	168	26.501	24.339	20.374	1.00	24.45	B	C
ATOM	2378	CB	LEU	B	168	25.605	23.091	20.428	1.00	21.23	B	C
ATOM	2379	CG	LEU	B	168	24.076	23.257	20.548	1.00	24.32	B	C
ATOM	2380	CD1	LEU	B	168	23.398	21.885	20.478	1.00	19.55	B	C
ATOM	2381	CD2	LEU	B	168	23.711	23.942	21.856	1.00	19.17	B	C
ATOM	2382	C	LEU	B	168	27.951	23.931	20.610	1.00	25.52	B	C
ATOM	2383	O	LEU	B	168	28.501	24.192	21.674	1.00	23.62	B	O
ATOM	2384	N	GLU	B	169	28.577	23.303	19.623	1.00	27.52	B	N
ATOM	2385	CA	GLU	B	169	29.948	22.844	19.809	1.00	32.03	B	C
ATOM	2386	CB	GLU	B	169	30.259	21.672	18.863	1.00	32.00	B	C
ATOM	2387	CG	GLU	B	169	29.545	21.711	17.535	1.00	35.49	B	C
ATOM	2388	CD	GLU	B	169	29.317	20.317	16.954	1.00	35.75	B	C
ATOM	2389	OE1	GLU	B	169	28.662	19.485	17.621	1.00	36.56	B	O
ATOM	2390	OE2	GLU	B	169	29.789	20.057	15.829	1.00	34.75	B	O
ATOM	2391	C	GLU	B	169	31.007	23.924	19.703	1.00	32.42	B	C
ATOM	2392	O	GLU	B	169	32.114	23.762	20.202	1.00	34.46	B	O

ATOM	2393	N	LYS	B	170	30.659	25.034	19.071	1.00	34.54	B	N
ATOM	2394	CA	LYS	B	170	31.585	26.142	18.934	1.00	34.41	B	C
ATOM	2395	CB	LYS	B	170	31.124	27.071	17.813	1.00	37.50	B	C
ATOM	2396	CG	LYS	B	170	32.090	28.190	17.512	1.00	41.65	B	C
ATOM	2397	CD	LYS	B	170	31.700	28.922	16.240	1.00	45.85	B	C
ATOM	2398	CE	LYS	B	170	31.944	28.064	15.005	1.00	48.44	B	C
ATOM	2399	NZ	LYS	B	170	33.402	27.794	14.811	1.00	48.66	B	N
ATOM	2400	C	LYS	B	170	31.639	26.899	20.253	1.00	34.06	B	C
ATOM	2401	O	LYS	B	170	32.694	27.395	20.651	1.00	31.09	B	O
ATOM	2402	N	ALA	B	171	30.496	26.966	20.937	1.00	33.89	B	N
ATOM	2403	CA	ALA	B	171	30.394	27.671	22.212	1.00	34.35	B	C
ATOM	2404	CB	ALA	B	171	28.955	28.087	22.467	1.00	31.71	B	C
ATOM	2405	C	ALA	B	171	30.914	26.869	23.398	1.00	36.33	B	C
ATOM	2406	O	ALA	B	171	30.973	27.374	24.517	1.00	37.82	B	O
ATOM	2407	N	GLY	B	172	31.288	25.619	23.168	1.00	37.10	B	N
ATOM	2408	CA	GLY	B	172	31.796	24.824	24.265	1.00	39.08	B	C
ATOM	2409	C	GLY	B	172	31.293	23.408	24.199	1.00	41.69	B	C
ATOM	2410	O	GLY	B	172	30.945	22.814	25.231	1.00	41.29	B	O
ATOM	2411	N	VAL	B	173	31.262	22.884	22.972	1.00	44.30	B	N
ATOM	2412	CA	VAL	B	173	30.807	21.528	22.670	1.00	44.96	B	C
ATOM	2413	CB	VAL	B	173	31.989	20.572	22.425	1.00	46.41	B	C
ATOM	2414	CG1	VAL	B	173	31.476	19.285	21.791	1.00	45.74	B	C
ATOM	2415	CG2	VAL	B	173	33.048	21.246	21.539	1.00	44.74	B	C
ATOM	2416	C	VAL	B	173	29.984	20.983	23.817	1.00	46.17	B	C
ATOM	2417	O	VAL	B	173	30.498	20.247	24.667	1.00	46.81	B	O
ATOM	2418	N	GLU	B	174	28.705	21.352	23.842	1.00	44.84	B	N
ATOM	2419	CA	GLU	B	174	27.841	20.912	24.911	1.00	42.70	B	C
ATOM	2420	CB	GLU	B	174	26.509	21.646	24.865	1.00	43.75	B	C
ATOM	2421	CG	GLU	B	174	26.485	22.871	25.754	1.00	44.96	B	C
ATOM	2422	CD	GLU	B	174	27.483	23.929	25.329	1.00	45.73	B	C
ATOM	2423	OE1	GLU	B	174	28.664	23.587	25.115	1.00	46.37	B	O
ATOM	2424	OE2	GLU	B	174	27.087	25.108	25.219	1.00	45.36	B	O
ATOM	2425	C	GLU	B	174	27.611	19.420	24.997	1.00	42.19	B	C
ATOM	2426	O	GLU	B	174	26.665	18.869	24.427	1.00	39.51	B	O
ATOM	2427	N	HIS	B	175	28.522	18.781	25.719	1.00	41.13	B	N
ATOM	2428	CA	HIS	B	175	28.458	17.365	26.001	1.00	40.20	B	C
ATOM	2429	CB	HIS	B	175	29.845	16.864	26.435	1.00	44.57	B	C
ATOM	2430	CG	HIS	B	175	29.880	15.420	26.837	1.00	49.02	B	C
ATOM	2431	CD2	HIS	B	175	30.422	14.337	26.228	1.00	50.48	B	C
ATOM	2432	ND1	HIS	B	175	29.305	14.954	28.001	1.00	51.44	B	N
ATOM	2433	CE1	HIS	B	175	29.490	13.648	28.091	1.00	51.08	B	C
ATOM	2434	NE2	HIS	B	175	30.165	13.249	27.027	1.00	51.29	B	N
ATOM	2435	C	HIS	B	175	27.493	17.408	27.185	1.00	37.70	B	C
ATOM	2436	O	HIS	B	175	26.942	16.394	27.604	1.00	37.04	B	O
ATOM	2437	N	GLN	B	176	27.282	18.621	27.692	1.00	35.01	B	N
ATOM	2438	CA	GLN	B	176	26.399	18.841	28.827	1.00	36.23	B	C
ATOM	2439	CB	GLN	B	176	26.846	20.066	29.624	1.00	37.61	B	C
ATOM	2440	CG	GLN	B	176	27.133	21.297	28.819	1.00	41.69	B	C
ATOM	2441	CD	GLN	B	176	27.294	22.516	29.710	1.00	46.57	B	C
ATOM	2442	OE1	GLN	B	176	27.841	23.549	29.298	1.00	49.05	B	O
ATOM	2443	NE2	GLN	B	176	26.807	22.406	30.942	1.00	47.86	B	N
ATOM	2444	C	GLN	B	176	24.921	18.970	28.473	1.00	34.56	B	C
ATOM	2445	O	GLN	B	176	24.063	18.678	29.299	1.00	34.08	B	O
ATOM	2446	N	LEU	B	177	24.624	19.419	27.259	1.00	33.44	B	N
ATOM	2447	CA	LEU	B	177	23.240	19.533	26.824	1.00	32.62	B	C
ATOM	2448	CB	LEU	B	177	23.163	20.178	25.433	1.00	33.83	B	C
ATOM	2449	CG	LEU	B	177	21.829	20.192	24.665	1.00	35.49	B	C
ATOM	2450	CD1	LEU	B	177	21.552	18.815	24.084	1.00	35.05	B	C
ATOM	2451	CD2	LEU	B	177	20.698	20.638	25.581	1.00	33.78	B	C
ATOM	2452	C	LEU	B	177	22.728	18.102	26.776	1.00	31.62	B	C
ATOM	2453	O	LEU	B	177	21.561	17.826	27.057	1.00	30.39	B	O
ATOM	2454	N	ARG	B	178	23.624	17.188	26.425	1.00	30.82	B	N
ATOM	2455	CA	ARG	B	178	23.265	15.784	26.357	1.00	32.73	B	C
ATOM	2456	CB	ARG	B	178	24.380	14.979	25.698	1.00	33.93	B	C
ATOM	2457	CG	ARG	B	178	24.492	15.194	24.207	1.00	39.47	B	C
ATOM	2458	CD	ARG	B	178	25.654	14.398	23.658	1.00	44.54	B	C
ATOM	2459	NE	ARG	B	178	25.537	12.989	24.018	1.00	47.63	B	N
ATOM	2460	CZ	ARG	B	178	26.501	12.098	23.838	1.00	48.23	B	C
ATOM	2461	NH1	ARG	B	178	27.651	12.476	23.302	1.00	49.75	B	N
ATOM	2462	NH2	ARG	B	178	26.316	10.835	24.192	1.00	49.72	B	N
ATOM	2463	C	ARG	B	178	22.998	15.241	27.753	1.00	32.47	B	C
ATOM	2464	O	ARG	B	178	21.976	14.597	27.995	1.00	33.18	B	O

ATOM	2465	N	ARG	B	179	23.912	15.506	28.676	1.00	30.61	B	N
ATOM	2466	CA	ARG	B	179	23.729	15.016	30.030	1.00	31.15	B	C
ATOM	2467	CB	ARG	B	179	24.965	15.320	30.880	1.00	34.46	B	C
ATOM	2468	CG	ARG	B	179	26.228	14.641	30.359	1.00	39.50	B	C
ATOM	2469	CD	ARG	B	179	26.988	13.929	31.471	1.00	43.76	B	C
ATOM	2470	NE	ARG	B	179	26.134	13.031	32.253	1.00	49.01	B	N
ATOM	2471	CZ	ARG	B	179	25.409	12.036	31.746	1.00	49.97	B	C
ATOM	2472	NH1	ARG	B	179	25.421	11.793	30.441	1.00	51.21	B	N
ATOM	2473	NH2	ARG	B	179	24.668	11.280	32.547	1.00	50.28	B	N
ATOM	2474	C	ARG	B	179	22.489	15.644	30.637	1.00	27.71	B	C
ATOM	2475	O	ARG	B	179	21.776	15.006	31.394	1.00	26.64	B	O
ATOM	2476	N	GLU	B	180	22.228	16.896	30.279	1.00	27.23	B	N
ATOM	2477	CA	GLU	B	180	21.070	17.620	30.782	1.00	26.36	B	C
ATOM	2478	CB	GLU	B	180	21.163	19.080	30.346	1.00	27.40	B	C
ATOM	2479	CG	GLU	B	180	20.452	20.047	31.271	1.00	30.43	B	C
ATOM	2480	CD	GLU	B	180	20.951	19.961	32.708	1.00	33.04	B	C
ATOM	2481	OE1	GLU	B	180	22.178	20.114	32.934	1.00	32.92	B	O
ATOM	2482	OE2	GLU	B	180	20.114	19.739	33.613	1.00	32.02	B	O
ATOM	2483	C	GLU	B	180	19.746	16.997	30.296	1.00	25.78	B	C
ATOM	2484	O	GLU	B	180	18.796	16.863	31.063	1.00	24.13	B	O
ATOM	2485	N	VAL	B	181	19.693	16.612	29.023	1.00	25.67	B	N
ATOM	2486	CA	VAL	B	181	18.494	16.002	28.453	1.00	27.08	B	C
ATOM	2487	CB	VAL	B	181	18.693	15.717	26.936	1.00	27.03	B	C
ATOM	2488	CG1	VAL	B	181	17.566	14.856	26.405	1.00	27.81	B	C
ATOM	2489	CG2	VAL	B	181	18.745	17.029	26.171	1.00	22.54	B	C
ATOM	2490	C	VAL	B	181	18.155	14.703	29.188	1.00	28.77	B	C
ATOM	2491	O	VAL	B	181	17.000	14.452	29.536	1.00	30.48	B	O
ATOM	2492	N	GLU	B	182	19.175	13.887	29.433	1.00	30.16	B	N
ATOM	2493	CA	GLU	B	182	19.024	12.615	30.139	1.00	29.83	B	C
ATOM	2494	CB	GLU	B	182	20.394	11.937	30.231	1.00	34.09	B	C
ATOM	2495	CG	GLU	B	182	20.452	10.614	30.983	1.00	40.35	B	C
ATOM	2496	CD	GLU	B	182	21.884	10.092	31.105	1.00	45.37	B	C
ATOM	2497	OE1	GLU	B	182	22.072	8.979	31.646	1.00	47.27	B	O
ATOM	2498	OE2	GLU	B	182	22.826	10.798	30.657	1.00	47.17	B	O
ATOM	2499	C	GLU	B	182	18.445	12.843	31.534	1.00	28.60	B	C
ATOM	2500	O	GLU	B	182	17.457	12.223	31.920	1.00	28.99	B	O
ATOM	2501	N	ILE	B	183	19.060	13.741	32.290	1.00	27.98	B	N
ATOM	2502	CA	ILE	B	183	18.593	14.056	33.636	1.00	28.08	B	C
ATOM	2503	CB	ILE	B	183	19.493	15.130	34.293	1.00	28.69	B	C
ATOM	2504	CG2	ILE	B	183	18.894	15.567	35.618	1.00	27.35	B	C
ATOM	2505	CG1	ILE	B	183	20.914	14.586	34.484	1.00	28.95	B	C
ATOM	2506	CD1	ILE	B	183	21.880	15.609	35.030	1.00	30.67	B	C
ATOM	2507	C	ILE	B	183	17.153	14.588	33.627	1.00	28.81	B	C
ATOM	2508	O	ILE	B	183	16.275	14.072	34.321	1.00	27.77	B	O
ATOM	2509	N	GLN	B	184	16.934	15.632	32.837	1.00	27.78	B	N
ATOM	2510	CA	GLN	B	184	15.635	16.283	32.721	1.00	29.40	B	C
ATOM	2511	CB	GLN	B	184	15.728	17.393	31.677	1.00	29.48	B	C
ATOM	2512	CG	GLN	B	184	15.084	18.695	32.085	1.00	33.57	B	C
ATOM	2513	CD	GLN	B	184	15.767	19.331	33.274	1.00	34.49	B	C
ATOM	2514	OE1	GLN	B	184	15.177	19.449	34.344	1.00	34.49	B	O
ATOM	2515	NE2	GLN	B	184	17.021	19.740	33.095	1.00	36.47	B	N
ATOM	2516	C	GLN	B	184	14.474	15.349	32.360	1.00	29.74	B	C
ATOM	2517	O	GLN	B	184	13.377	15.473	32.899	1.00	29.32	B	O
ATOM	2518	N	SER	B	185	14.714	14.411	31.455	1.00	30.43	B	N
ATOM	2519	CA	SER	B	185	13.659	13.497	31.024	1.00	31.44	B	C
ATOM	2520	CB	SER	B	185	14.123	12.710	29.801	1.00	29.48	B	C
ATOM	2521	OG	SER	B	185	15.188	11.853	30.147	1.00	33.05	B	O
ATOM	2522	C	SER	B	185	13.151	12.524	32.093	1.00	32.12	B	C
ATOM	2523	O	SER	B	185	12.156	11.842	31.884	1.00	31.84	B	O
ATOM	2524	N	HIS	B	186	13.818	12.463	33.237	1.00	33.65	B	N
ATOM	2525	CA	HIS	B	186	13.391	11.564	34.305	1.00	34.39	B	C
ATOM	2526	CB	HIS	B	186	14.582	10.731	34.781	1.00	36.84	B	C
ATOM	2527	CG	HIS	B	186	15.052	9.729	33.773	1.00	39.30	B	C
ATOM	2528	CD2	HIS	B	186	14.363	8.961	32.893	1.00	40.21	B	C
ATOM	2529	ND1	HIS	B	186	16.384	9.432	33.581	1.00	39.62	B	N
ATOM	2530	CE1	HIS	B	186	16.497	8.528	32.623	1.00	42.04	B	C
ATOM	2531	NE2	HIS	B	186	15.286	8.225	32.189	1.00	42.20	B	N
ATOM	2532	C	HIS	B	186	12.758	12.295	35.487	1.00	34.27	B	C
ATOM	2533	O	HIS	B	186	12.296	11.667	36.442	1.00	34.94	B	O
ATOM	2534	N	LEU	B	187	12.745	13.621	35.423	1.00	32.72	B	N
ATOM	2535	CA	LEU	B	187	12.162	14.441	36.476	1.00	31.38	B	C
ATOM	2536	CB	LEU	B	187	12.798	15.835	36.466	1.00	30.82	B	C

ATOM	2537	CG	LEU	B	187	14.074	16.108	37.274	1.00	31.43	B	C
ATOM	2538	CD1	LEU	B	187	14.997	14.911	37.294	1.00	32.58	B	C
ATOM	2539	CD2	LEU	B	187	14.764	17.317	36.686	1.00	31.34	B	C
ATOM	2540	C	LEU	B	187	10.659	14.569	36.248	1.00	31.86	B	C
ATOM	2541	O	LEU	B	187	10.214	14.797	35.121	1.00	30.47	B	O
ATOM	2542	N	ALA	B	188	9.881	14.413	37.316	1.00	31.25	B	N
ATOM	2543	CA	ALA	B	188	8.429	14.530	37.230	1.00	30.44	B	C
ATOM	2544	CB	ALA	B	188	7.789	13.148	37.091	1.00	29.88	B	C
ATOM	2545	C	ALA	B	188	7.912	15.237	38.481	1.00	29.21	B	C
ATOM	2546	O	ALA	B	188	7.862	14.651	39.559	1.00	28.34	B	O
ATOM	2547	N	HIS	B	189	7.538	16.504	38.319	1.00	28.72	B	N
ATOM	2548	CA	HIS	B	189	7.032	17.326	39.412	1.00	27.13	B	C
ATOM	2549	CB	HIS	B	189	8.205	17.925	40.201	1.00	27.59	B	C
ATOM	2550	CG	HIS	B	189	7.799	18.662	41.442	1.00	24.39	B	C
ATOM	2551	CD2	HIS	B	189	7.993	18.377	42.752	1.00	25.28	B	C
ATOM	2552	ND1	HIS	B	189	7.122	19.859	41.410	1.00	26.03	B	N
ATOM	2553	CE1	HIS	B	189	6.919	20.283	42.646	1.00	24.93	B	C
ATOM	2554	NE2	HIS	B	189	7.438	19.402	43.479	1.00	23.51	B	N
ATOM	2555	C	HIS	B	189	6.193	18.431	38.787	1.00	26.49	B	C
ATOM	2556	O	HIS	B	189	6.562	18.998	37.766	1.00	26.44	B	O
ATOM	2557	N	PRO	B	190	5.049	18.760	39.402	1.00	26.98	B	N
ATOM	2558	CD	PRO	B	190	4.548	18.263	40.699	1.00	25.70	B	C
ATOM	2559	CA	PRO	B	190	4.177	19.807	38.863	1.00	24.70	B	C
ATOM	2560	CB	PRO	B	190	2.998	19.811	39.846	1.00	25.70	B	C
ATOM	2561	CG	PRO	B	190	3.633	19.382	41.139	1.00	26.97	B	C
ATOM	2562	C	PRO	B	190	4.814	21.191	38.682	1.00	24.45	B	C
ATOM	2563	O	PRO	B	190	4.378	21.966	37.832	1.00	24.60	B	O
ATOM	2564	N	ASN	B	191	5.842	21.506	39.464	1.00	22.38	B	N
ATOM	2565	CA	ASN	B	191	6.481	22.809	39.346	1.00	21.54	B	C
ATOM	2566	CB	ASN	B	191	6.713	23.408	40.730	1.00	21.05	B	C
ATOM	2567	CG	ASN	B	191	5.436	23.575	41.495	1.00	19.72	B	C
ATOM	2568	OD1	ASN	B	191	4.567	24.371	41.121	1.00	19.90	B	O
ATOM	2569	ND2	ASN	B	191	5.299	22.815	42.571	1.00	20.48	B	N
ATOM	2570	C	ASN	B	191	7.793	22.801	38.564	1.00	21.58	B	C
ATOM	2571	O	ASN	B	191	8.627	23.699	38.720	1.00	19.27	B	O
ATOM	2572	N	ILE	B	192	7.964	21.787	37.722	1.00	20.97	B	N
ATOM	2573	CA	ILE	B	192	9.154	21.674	36.880	1.00	21.01	B	C
ATOM	2574	CB	ILE	B	192	10.064	20.494	37.331	1.00	21.26	B	C
ATOM	2575	CG2	ILE	B	192	11.219	20.288	36.331	1.00	19.48	B	C
ATOM	2576	CG1	ILE	B	192	10.613	20.770	38.733	1.00	21.57	B	C
ATOM	2577	CD1	ILE	B	192	11.462	19.627	39.299	1.00	23.94	B	C
ATOM	2578	C	ILE	B	192	8.667	21.432	35.453	1.00	19.86	B	C
ATOM	2579	O	ILE	B	192	7.908	20.497	35.210	1.00	22.96	B	O
ATOM	2580	N	LEU	B	193	9.082	22.282	34.519	1.00	20.26	B	N
ATOM	2581	CA	LEU	B	193	8.669	22.142	33.124	1.00	21.42	B	C
ATOM	2582	CB	LEU	B	193	9.307	23.234	32.268	1.00	22.27	B	C
ATOM	2583	CG	LEU	B	193	8.681	23.436	30.883	1.00	23.28	B	C
ATOM	2584	CD1	LEU	B	193	7.245	23.930	31.030	1.00	21.92	B	C
ATOM	2585	CD2	LEU	B	193	9.495	24.445	30.101	1.00	19.52	B	C
ATOM	2586	C	LEU	B	193	9.041	20.763	32.565	1.00	21.67	B	C
ATOM	2587	O	LEU	B	193	10.199	20.350	32.598	1.00	18.44	B	O
ATOM	2588	N	ARG	B	194	8.041	20.069	32.036	1.00	21.75	B	N
ATOM	2589	CA	ARG	B	194	8.215	18.732	31.482	1.00	23.01	B	C
ATOM	2590	CB	ARG	B	194	6.841	18.096	31.268	1.00	25.81	B	C
ATOM	2591	CG	ARG	B	194	6.788	16.596	31.448	1.00	32.81	B	C
ATOM	2592	CD	ARG	B	194	6.817	16.240	32.921	1.00	37.46	B	C
ATOM	2593	NE	ARG	B	194	6.281	14.904	33.176	1.00	44.90	B	N
ATOM	2594	CZ	ARG	B	194	5.012	14.542	32.974	1.00	47.96	B	C
ATOM	2595	NH1	ARG	B	194	4.125	15.418	32.508	1.00	48.71	B	N
ATOM	2596	NH2	ARG	B	194	4.626	13.299	33.247	1.00	48.22	B	N
ATOM	2597	C	ARG	B	194	8.981	18.673	30.159	1.00	21.93	B	C
ATOM	2598	O	ARG	B	194	8.821	19.538	29.292	1.00	19.59	B	O
ATOM	2599	N	LEU	B	195	9.819	17.647	30.021	1.00	21.33	B	N
ATOM	2600	CA	LEU	B	195	10.567	17.403	28.788	1.00	22.76	B	C
ATOM	2601	CB	LEU	B	195	12.053	17.148	29.069	1.00	22.81	B	C
ATOM	2602	CG	LEU	B	195	13.078	17.437	27.959	1.00	24.02	B	C
ATOM	2603	CD1	LEU	B	195	14.267	16.498	28.140	1.00	21.85	B	C
ATOM	2604	CD2	LEU	B	195	12.483	17.251	26.563	1.00	23.51	B	C
ATOM	2605	C	LEU	B	195	9.921	16.119	28.274	1.00	22.36	B	C
ATOM	2606	O	LEU	B	195	10.110	15.056	28.861	1.00	22.57	B	O
ATOM	2607	N	TYR	B	196	9.145	16.215	27.201	1.00	22.31	B	N
ATOM	2608	CA	TYR	B	196	8.453	15.050	26.651	1.00	22.19	B	C

ATOM	2609	CB	TYR	B	196	7.281	15.490	25.768	1.00	23.58	B	C
ATOM	2610	CG	TYR	B	196	6.155	16.146	26.519	1.00	23.96	B	C
ATOM	2611	CD1	TYR	B	196	5.772	17.460	26.238	1.00	25.04	B	C
ATOM	2612	CE1	TYR	B	196	4.728	18.071	26.937	1.00	24.87	B	C
ATOM	2613	CD2	TYR	B	196	5.467	15.457	27.515	1.00	25.05	B	C
ATOM	2614	CE2	TYR	B	196	4.426	16.056	28.217	1.00	25.56	B	C
ATOM	2615	CZ	TYR	B	196	4.062	17.361	27.923	1.00	25.01	B	C
ATOM	2616	OH	TYR	B	196	3.023	17.944	28.612	1.00	29.27	B	O
ATOM	2617	C	TYR	B	196	9.333	14.108	25.851	1.00	22.57	B	C
ATOM	2618	O	TYR	B	196	9.132	12.898	25.873	1.00	23.50	B	O
ATOM	2619	N	GLY	B	197	10.294	14.663	25.124	1.00	22.59	B	N
ATOM	2620	CA	GLY	B	197	11.180	13.841	24.332	1.00	20.31	B	C
ATOM	2621	C	GLY	B	197	12.161	14.702	23.572	1.00	23.62	B	C
ATOM	2622	O	GLY	B	197	12.220	15.919	23.772	1.00	24.47	B	O
ATOM	2623	N	TYR	B	198	12.935	14.078	22.695	1.00	23.97	B	N
ATOM	2624	CA	TYR	B	198	13.903	14.810	21.900	1.00	27.71	B	C
ATOM	2625	CB	TYR	B	198	15.140	15.125	22.735	1.00	31.42	B	C
ATOM	2626	CG	TYR	B	198	15.966	13.915	23.087	1.00	36.13	B	C
ATOM	2627	CD1	TYR	B	198	17.100	13.584	22.349	1.00	37.59	B	C
ATOM	2628	CE1	TYR	B	198	17.863	12.466	22.667	1.00	40.01	B	C
ATOM	2629	CD2	TYR	B	198	15.611	13.096	24.158	1.00	38.85	B	C
ATOM	2630	CE2	TYR	B	198	16.364	11.977	24.485	1.00	40.86	B	C
ATOM	2631	CZ	TYR	B	198	17.489	11.667	23.734	1.00	41.45	B	C
ATOM	2632	OH	TYR	B	198	18.232	10.550	24.049	1.00	46.15	B	O
ATOM	2633	C	TYR	B	198	14.293	13.982	20.699	1.00	26.60	B	C
ATOM	2634	O	TYR	B	198	13.951	12.812	20.611	1.00	26.01	B	O
ATOM	2635	N	PHE	B	199	15.000	14.599	19.767	1.00	27.65	B	N
ATOM	2636	CA	PHE	B	199	15.443	13.904	18.572	1.00	27.79	B	C
ATOM	2637	CB	PHE	B	199	14.233	13.426	17.749	1.00	27.11	B	C
ATOM	2638	CG	PHE	B	199	13.388	14.540	17.161	1.00	27.89	B	C
ATOM	2639	CD1	PHE	B	199	13.637	15.019	15.876	1.00	27.86	B	C
ATOM	2640	CD2	PHE	B	199	12.310	15.064	17.868	1.00	27.14	B	C
ATOM	2641	CE1	PHE	B	199	12.894	15.996	15.301	1.00	26.93	B	C
ATOM	2642	CE2	PHE	B	199	11.492	16.040	17.303	1.00	26.16	B	C
ATOM	2643	CZ	PHE	B	199	11.750	16.505	16.015	1.00	27.17	B	C
ATOM	2644	C	PHE	B	199	16.297	14.860	17.767	1.00	28.08	B	C
ATOM	2645	O	PHE	B	199	16.345	16.049	18.073	1.00	28.24	B	O
ATOM	2646	N	HIS	B	200	16.993	14.353	16.758	1.00	27.87	B	N
ATOM	2647	CA	HIS	B	200	17.806	15.238	15.938	1.00	29.75	B	C
ATOM	2648	CB	HIS	B	200	19.100	15.594	16.681	1.00	33.26	B	C
ATOM	2649	CG	HIS	B	200	19.948	14.418	17.048	1.00	34.79	B	C
ATOM	2650	CD2	HIS	B	200	21.287	14.230	16.965	1.00	36.25	B	C
ATOM	2651	ND1	HIS	B	200	19.439	13.288	17.648	1.00	35.92	B	N
ATOM	2652	CE1	HIS	B	200	20.427	12.454	17.921	1.00	37.18	B	C
ATOM	2653	NE2	HIS	B	200	21.559	13.003	17.517	1.00	36.60	B	N
ATOM	2654	C	HIS	B	200	18.116	14.715	14.538	1.00	27.95	B	C
ATOM	2655	O	HIS	B	200	17.752	13.591	14.187	1.00	26.05	B	O
ATOM	2656	N	ASP	B	201	18.725	15.571	13.721	1.00	26.67	B	N
ATOM	2657	CA	ASP	B	201	19.138	15.186	12.377	1.00	25.20	B	C
ATOM	2658	CB	ASP	B	201	18.335	15.916	11.282	1.00	23.68	B	C
ATOM	2659	CG	ASP	B	201	18.264	17.424	11.483	1.00	25.88	B	C
ATOM	2660	OD1	ASP	B	201	19.294	18.047	11.802	1.00	23.44	B	O
ATOM	2661	OD2	ASP	B	201	17.166	17.998	11.290	1.00	26.10	B	O
ATOM	2662	C	ASP	B	201	20.627	15.505	12.299	1.00	24.36	B	C
ATOM	2663	O	ASP	B	201	21.263	15.653	13.339	1.00	24.08	B	O
ATOM	2664	N	ALA	B	202	21.184	15.617	11.096	1.00	22.49	B	N
ATOM	2665	CA	ALA	B	202	22.615	15.887	10.946	1.00	22.92	B	C
ATOM	2666	CB	ALA	B	202	23.038	15.661	9.485	1.00	21.85	B	C
ATOM	2667	C	ALA	B	202	23.106	17.263	11.420	1.00	22.02	B	C
ATOM	2668	O	ALA	B	202	24.289	17.437	11.710	1.00	19.11	B	O
ATOM	2669	N	ALA	B	203	22.212	18.237	11.520	1.00	21.84	B	N
ATOM	2670	CA	ALA	B	203	22.654	19.564	11.935	1.00	20.59	B	C
ATOM	2671	CB	ALA	B	203	22.661	20.502	10.718	1.00	18.98	B	C
ATOM	2672	C	ALA	B	203	21.902	20.213	13.095	1.00	17.95	B	C
ATOM	2673	O	ALA	B	203	22.321	21.262	13.583	1.00	19.24	B	O
ATOM	2674	N	ARG	B	204	20.825	19.595	13.568	1.00	17.86	B	N
ATOM	2675	CA	ARG	B	204	20.060	20.197	14.660	1.00	19.08	B	C
ATOM	2676	CB	ARG	B	204	18.849	20.964	14.111	1.00	23.11	B	C
ATOM	2677	CG	ARG	B	204	19.083	21.702	12.813	1.00	24.65	B	C
ATOM	2678	CD	ARG	B	204	17.793	22.345	12.317	1.00	31.21	B	C
ATOM	2679	NE	ARG	B	204	17.847	22.663	10.890	1.00	36.40	B	N
ATOM	2680	CZ	ARG	B	204	17.679	21.773	9.911	1.00	38.70	B	C

ATOM	2681	NH1	ARG	B	204	17.752	22.161	8.644	1.00	41.01	B	N
ATOM	2682	NH2	ARG	B	204	17.419	20.500	10.191	1.00	38.76	B	N
ATOM	2683	C	ARG	B	204	19.547	19.228	15.711	1.00	18.39	B	C
ATOM	2684	O	ARG	B	204	19.463	18.030	15.492	1.00	18.56	B	O
ATOM	2685	N	VAL	B	205	19.199	19.767	16.870	1.00	18.68	B	N
ATOM	2686	CA	VAL	B	205	18.649	18.958	17.949	1.00	18.67	B	C
ATOM	2687	CB	VAL	B	205	19.551	18.984	19.201	1.00	18.98	B	C
ATOM	2688	CG1	VAL	B	205	18.933	18.135	20.301	1.00	19.79	B	C
ATOM	2689	CG2	VAL	B	205	20.947	18.472	18.852	1.00	15.84	B	C
ATOM	2690	C	VAL	B	205	17.290	19.572	18.282	1.00	19.14	B	C
ATOM	2691	O	VAL	B	205	17.182	20.796	18.405	1.00	21.54	B	O
ATOM	2692	N	TYR	B	206	16.263	18.731	18.396	1.00	17.89	B	N
ATOM	2693	CA	TYR	B	206	14.910	19.193	18.709	1.00	19.04	B	C
ATOM	2694	CB	TYR	B	206	13.891	18.696	17.674	1.00	18.60	B	C
ATOM	2695	CG	TYR	B	206	14.228	19.017	16.240	1.00	18.39	B	C
ATOM	2696	CD1	TYR	B	206	15.207	18.293	15.565	1.00	21.42	B	C
ATOM	2697	CE1	TYR	B	206	15.542	18.578	14.244	1.00	21.55	B	C
ATOM	2698	CD2	TYR	B	206	13.576	20.052	15.555	1.00	19.46	B	C
ATOM	2699	CE2	TYR	B	206	13.907	20.352	14.216	1.00	21.97	B	C
ATOM	2700	CZ	TYR	B	206	14.898	19.602	13.573	1.00	23.91	B	C
ATOM	2701	OH	TYR	B	206	15.267	19.858	12.269	1.00	26.45	B	O
ATOM	2702	C	TYR	B	206	14.459	18.705	20.073	1.00	19.50	B	C
ATOM	2703	O	TYR	B	206	14.538	17.508	20.373	1.00	21.94	B	O
ATOM	2704	N	LEU	B	207	13.985	19.633	20.897	1.00	16.85	B	N
ATOM	2705	CA	LEU	B	207	13.491	19.291	22.224	1.00	17.98	B	C
ATOM	2706	CB	LEU	B	207	14.181	20.161	23.286	1.00	16.72	B	C
ATOM	2707	CG	LEU	B	207	15.722	20.138	23.321	1.00	19.44	B	C
ATOM	2708	CD1	LEU	B	207	16.216	21.031	24.461	1.00	19.09	B	C
ATOM	2709	CD2	LEU	B	207	16.226	18.707	23.519	1.00	19.58	B	C
ATOM	2710	C	LEU	B	207	11.973	19.535	22.225	1.00	17.04	B	C
ATOM	2711	O	LEU	B	207	11.513	20.588	21.803	1.00	18.06	B	O
ATOM	2712	N	ILE	B	208	11.205	18.547	22.674	1.00	18.23	B	N
ATOM	2713	CA	ILE	B	208	9.747	18.653	22.727	1.00	16.54	B	C
ATOM	2714	CB	ILE	B	208	9.093	17.336	22.272	1.00	16.55	B	C
ATOM	2715	CG2	ILE	B	208	7.568	17.474	22.238	1.00	14.96	B	C
ATOM	2716	CG1	ILE	B	208	9.614	16.978	20.872	1.00	20.37	B	C
ATOM	2717	CD1	ILE	B	208	9.149	15.613	20.347	1.00	21.43	B	C
ATOM	2718	C	ILE	B	208	9.412	18.969	24.179	1.00	17.23	B	C
ATOM	2719	O	ILE	B	208	9.625	18.144	25.081	1.00	16.63	B	O
ATOM	2720	N	LEU	B	209	8.871	20.166	24.401	1.00	16.12	B	N
ATOM	2721	CA	LEU	B	209	8.577	20.630	25.752	1.00	17.56	B	C
ATOM	2722	CB	LEU	B	209	9.472	21.830	26.063	1.00	17.90	B	C
ATOM	2723	CG	LEU	B	209	10.978	21.577	25.959	1.00	19.46	B	C
ATOM	2724	CD1	LEU	B	209	11.664	22.798	25.379	1.00	19.75	B	C
ATOM	2725	CD2	LEU	B	209	11.556	21.215	27.336	1.00	19.17	B	C
ATOM	2726	C	LEU	B	209	7.144	21.018	26.084	1.00	18.62	B	C
ATOM	2727	O	LEU	B	209	6.348	21.346	25.202	1.00	18.84	B	O
ATOM	2728	N	GLU	B	210	6.844	20.984	27.381	1.00	16.02	B	N
ATOM	2729	CA	GLU	B	210	5.549	21.382	27.898	1.00	17.17	B	C
ATOM	2730	CB	GLU	B	210	5.496	21.128	29.409	1.00	16.24	B	C
ATOM	2731	CG	GLU	B	210	4.275	21.705	30.100	1.00	17.66	B	C
ATOM	2732	CD	GLU	B	210	4.319	21.542	31.615	1.00	19.26	B	C
ATOM	2733	OE1	GLU	B	210	3.396	22.037	32.298	1.00	19.17	B	O
ATOM	2734	OE2	GLU	B	210	5.273	20.919	32.126	1.00	18.51	B	O
ATOM	2735	C	GLU	B	210	5.419	22.881	27.619	1.00	17.58	B	C
ATOM	2736	O	GLU	B	210	6.386	23.640	27.787	1.00	17.15	B	O
ATOM	2737	N	TYR	B	211	4.239	23.301	27.177	1.00	17.46	B	N
ATOM	2738	CA	TYR	B	211	3.975	24.707	26.875	1.00	17.27	B	C
ATOM	2739	CB	TYR	B	211	2.915	24.830	25.771	1.00	17.32	B	C
ATOM	2740	CG	TYR	B	211	2.598	26.265	25.406	1.00	18.99	B	C
ATOM	2741	CD1	TYR	B	211	3.601	27.115	24.953	1.00	18.89	B	C
ATOM	2742	CE1	TYR	B	211	3.337	28.443	24.637	1.00	18.07	B	C
ATOM	2743	CD2	TYR	B	211	1.300	26.783	25.536	1.00	19.53	B	C
ATOM	2744	CE2	TYR	B	211	1.025	28.124	25.215	1.00	17.93	B	C
ATOM	2745	CZ	TYR	B	211	2.058	28.943	24.766	1.00	19.57	B	C
ATOM	2746	OH	TYR	B	211	1.837	30.268	24.435	1.00	21.28	B	O
ATOM	2747	C	TYR	B	211	3.488	25.437	28.119	1.00	17.08	B	C
ATOM	2748	O	TYR	B	211	2.676	24.905	28.880	1.00	20.12	B	O
ATOM	2749	N	ALA	B	212	3.977	26.657	28.315	1.00	16.19	B	N
ATOM	2750	CA	ALA	B	212	3.619	27.487	29.470	1.00	16.51	B	C
ATOM	2751	CB	ALA	B	212	4.882	27.927	30.202	1.00	15.30	B	C

ATOM	2752	C	ALA	B	212	2.856	28.705	28.952	1.00	17.50	B	C
ATOM	2753	O	ALA	B	212	3.450	29.726	28.596	1.00	18.16	B	O
ATOM	2754	N	PRO	B	213	1.520	28.618	28.925	1.00	17.93	B	N
ATOM	2755	CD	PRO	B	213	0.728	27.494	29.458	1.00	16.26	B	C
ATOM	2756	CA	PRO	B	213	0.651	29.693	28.437	1.00	18.73	B	C
ATOM	2757	CB	PRO	B	213	-0.758	29.108	28.604	1.00	17.80	B	C
ATOM	2758	CG	PRO	B	213	-0.609	28.146	29.724	1.00	19.64	B	C
ATOM	2759	C	PRO	B	213	0.761	31.115	28.984	1.00	19.83	B	C
ATOM	2760	O	PRO	B	213	0.513	32.063	28.245	1.00	20.80	B	O
ATOM	2761	N	LEU	B	214	1.128	31.288	30.250	1.00	20.66	B	N
ATOM	2762	CA	LEU	B	214	1.211	32.640	30.798	1.00	20.06	B	C
ATOM	2763	CB	LEU	B	214	0.709	32.647	32.255	1.00	19.58	B	C
ATOM	2764	CG	LEU	B	214	-0.812	32.790	32.467	1.00	22.04	B	C
ATOM	2765	CD1	LEU	B	214	-1.576	31.829	31.576	1.00	23.11	B	C
ATOM	2766	CD2	LEU	B	214	-1.161	32.538	33.926	1.00	22.72	B	C
ATOM	2767	C	LEU	B	214	2.572	33.346	30.686	1.00	21.48	B	C
ATOM	2768	O	LEU	B	214	2.749	34.451	31.200	1.00	23.25	B	O
ATOM	2769	N	GLY	B	215	3.533	32.724	30.013	1.00	21.00	B	N
ATOM	2770	CA	GLY	B	215	4.825	33.368	29.847	1.00	21.31	B	C
ATOM	2771	C	GLY	B	215	5.790	33.299	31.023	1.00	23.13	B	C
ATOM	2772	O	GLY	B	215	5.657	32.448	31.904	1.00	23.73	B	O
ATOM	2773	N	THR	B	216	6.758	34.214	31.042	1.00	22.29	B	N
ATOM	2774	CA	THR	B	216	7.779	34.238	32.088	1.00	23.81	B	C
ATOM	2775	CB	THR	B	216	9.127	34.692	31.517	1.00	23.63	B	C
ATOM	2776	OG1	THR	B	216	9.090	36.102	31.277	1.00	25.10	B	O
ATOM	2777	CG2	THR	B	216	9.409	33.987	30.199	1.00	22.17	B	C
ATOM	2778	C	THR	B	216	7.461	35.125	33.291	1.00	23.33	B	C
ATOM	2779	O	THR	B	216	6.712	36.100	33.191	1.00	20.98	B	O
ATOM	2780	N	VAL	B	217	8.036	34.774	34.435	1.00	22.90	B	N
ATOM	2781	CA	VAL	B	217	7.827	35.554	35.651	1.00	24.21	B	C
ATOM	2782	CB	VAL	B	217	8.470	34.857	36.867	1.00	23.26	B	C
ATOM	2783	CG1	VAL	B	217	8.387	35.740	38.109	1.00	22.26	B	C
ATOM	2784	CG2	VAL	B	217	7.763	33.552	37.110	1.00	22.25	B	C
ATOM	2785	C	VAL	B	217	8.439	36.935	35.449	1.00	23.65	B	C
ATOM	2786	O	VAL	B	217	7.922	37.933	35.932	1.00	23.81	B	O
ATOM	2787	N	TYR	B	218	9.536	36.967	34.708	1.00	25.98	B	N
ATOM	2788	CA	TYR	B	218	10.247	38.193	34.395	1.00	29.23	B	C
ATOM	2789	CB	TYR	B	218	11.395	37.865	33.437	1.00	33.60	B	C
ATOM	2790	CG	TYR	B	218	12.225	39.040	32.974	1.00	37.23	B	C
ATOM	2791	CD1	TYR	B	218	11.965	39.661	31.753	1.00	39.24	B	C
ATOM	2792	CE1	TYR	B	218	12.756	40.710	31.296	1.00	40.90	B	C
ATOM	2793	CD2	TYR	B	218	13.296	39.503	33.733	1.00	39.21	B	C
ATOM	2794	CE2	TYR	B	218	14.096	40.551	33.285	1.00	41.41	B	C
ATOM	2795	CZ	TYR	B	218	13.819	41.149	32.065	1.00	42.06	B	C
ATOM	2796	OH	TYR	B	218	14.609	42.175	31.607	1.00	43.77	B	O
ATOM	2797	C	TYR	B	218	9.302	39.228	33.788	1.00	30.16	B	C
ATOM	2798	O	TYR	B	218	9.259	40.368	34.242	1.00	31.95	B	O
ATOM	2799	N	ALA	B	219	8.540	38.831	32.770	1.00	30.65	B	N
ATOM	2800	CA	ALA	B	219	7.589	39.736	32.123	1.00	29.66	B	C
ATOM	2801	CB	ALA	B	219	6.906	39.026	30.967	1.00	28.94	B	C
ATOM	2802	C	ALA	B	219	6.542	40.257	33.118	1.00	29.78	B	C
ATOM	2803	O	ALA	B	219	6.199	41.438	33.110	1.00	28.08	B	O
ATOM	2804	N	GLU	B	220	6.027	39.371	33.964	1.00	30.79	B	N
ATOM	2805	CA	GLU	B	220	5.037	39.753	34.968	1.00	34.09	B	C
ATOM	2806	CB	GLU	B	220	4.587	38.529	35.766	1.00	36.73	B	C
ATOM	2807	CG	GLU	B	220	3.344	37.838	35.251	1.00	43.32	B	C
ATOM	2808	CD	GLU	B	220	2.073	38.618	35.542	1.00	46.85	B	C
ATOM	2809	OE1	GLU	B	220	1.801	39.613	34.835	1.00	48.71	B	O
ATOM	2810	OE2	GLU	B	220	1.350	38.237	36.489	1.00	48.33	B	O
ATOM	2811	C	GLU	B	220	5.618	40.785	35.934	1.00	34.92	B	C
ATOM	2812	O	GLU	B	220	4.956	41.755	36.296	1.00	36.60	B	O
ATOM	2813	N	LEU	B	221	6.858	40.569	36.356	1.00	34.26	B	N
ATOM	2814	CA	LEU	B	221	7.505	41.482	37.286	1.00	34.78	B	C
ATOM	2815	CB	LEU	B	221	8.920	40.995	37.621	1.00	33.24	B	C
ATOM	2816	CG	LEU	B	221	9.646	41.761	38.735	1.00	32.72	B	C
ATOM	2817	CD1	LEU	B	221	8.807	41.773	40.010	1.00	30.46	B	C
ATOM	2818	CD2	LEU	B	221	10.996	41.112	38.988	1.00	32.35	B	C
ATOM	2819	C	LEU	B	221	7.565	42.880	36.693	1.00	34.90	B	C
ATOM	2820	O	LEU	B	221	7.275	43.864	37.374	1.00	32.14	B	O
ATOM	2821	N	GLN	B	222	7.941	42.961	35.419	1.00	35.21	B	N
ATOM	2822	CA	GLN	B	222	8.026	44.241	34.735	1.00	37.12	B	C

ATOM	2823	CB	GLN	B	222	8.563	44.044	33.319	1.00	39.87	B	C
ATOM	2824	CG	GLN	B	222	9.945	43.424	33.287	1.00	44.00	B	C
ATOM	2825	CD	GLN	B	222	10.690	43.723	32.004	1.00	47.25	B	C
ATOM	2826	OE1	GLN	B	222	10.220	43.410	30.907	1.00	49.30	B	O
ATOM	2827	NE2	GLN	B	222	11.864	44.333	32.135	1.00	48.03	B	N
ATOM	2828	C	GLN	B	222	6.684	44.972	34.687	1.00	36.68	B	C
ATOM	2829	O	GLN	B	222	6.634	46.184	34.865	1.00	37.49	B	O
ATOM	2830	N	LYS	B	223	5.597	44.241	34.461	1.00	35.79	B	N
ATOM	2831	CA	LYS	B	223	4.277	44.859	34.406	1.00	36.52	B	C
ATOM	2832	CB	LYS	B	223	3.237	43.868	33.875	1.00	37.92	B	C
ATOM	2833	CG	LYS	B	223	3.354	43.561	32.389	1.00	39.91	B	C
ATOM	2834	CD	LYS	B	223	2.292	42.560	31.944	1.00	42.68	B	C
ATOM	2835	CE	LYS	B	223	0.886	43.140	32.033	1.00	43.66	B	C
ATOM	2836	NZ	LYS	B	223	0.693	44.275	31.079	1.00	46.03	B	N
ATOM	2837	C	LYS	B	223	3.792	45.402	35.749	1.00	36.84	B	C
ATOM	2838	O	LYS	B	223	3.357	46.550	35.833	1.00	38.21	B	O
ATOM	2839	N	LEU	B	224	3.860	44.580	36.795	1.00	35.10	B	N
ATOM	2840	CA	LEU	B	224	3.398	44.988	38.122	1.00	33.56	B	C
ATOM	2841	CB	LEU	B	224	2.929	43.762	38.913	1.00	33.55	B	C
ATOM	2842	CG	LEU	B	224	1.871	42.852	38.282	1.00	34.89	B	C
ATOM	2843	CD1	LEU	B	224	1.619	41.658	39.189	1.00	33.24	B	C
ATOM	2844	CD2	LEU	B	224	0.589	43.630	38.059	1.00	34.60	B	C
ATOM	2845	C	LEU	B	224	4.452	45.735	38.939	1.00	32.05	B	C
ATOM	2846	O	LEU	B	224	4.141	46.297	39.989	1.00	32.92	B	O
ATOM	2847	N	SER	B	225	5.691	45.723	38.455	1.00	30.59	B	N
ATOM	2848	CA	SER	B	225	6.826	46.380	39.112	1.00	31.41	B	C
ATOM	2849	CB	SER	B	225	6.449	47.792	39.549	1.00	32.21	B	C
ATOM	2850	OG	SER	B	225	7.615	48.537	39.843	1.00	34.55	B	O
ATOM	2851	C	SER	B	225	7.361	45.585	40.318	1.00	31.23	B	C
ATOM	2852	O	SER	B	225	8.556	45.589	40.599	1.00	30.58	B	O
ATOM	2853	N	LYS	B	226	6.466	44.921	41.035	1.00	30.59	B	N
ATOM	2854	CA	LYS	B	226	6.851	44.096	42.173	1.00	31.60	B	C
ATOM	2855	CB	LYS	B	226	7.535	44.924	43.273	1.00	32.62	B	C
ATOM	2856	CG	LYS	B	226	6.733	46.065	43.866	1.00	33.34	B	C
ATOM	2857	CD	LYS	B	226	7.482	46.606	45.085	1.00	37.58	B	C
ATOM	2858	CE	LYS	B	226	6.839	47.858	45.658	1.00	39.62	B	C
ATOM	2859	NZ	LYS	B	226	7.074	49.049	44.786	1.00	41.42	B	N
ATOM	2860	C	LYS	B	226	5.620	43.400	42.707	1.00	29.47	B	C
ATOM	2861	O	LYS	B	226	4.501	43.795	42.391	1.00	29.83	B	O
ATOM	2862	N	PHE	B	227	5.821	42.355	43.500	1.00	28.21	B	N
ATOM	2863	CA	PHE	B	227	4.702	41.597	44.039	1.00	26.85	B	C
ATOM	2864	CB	PHE	B	227	4.928	40.091	43.833	1.00	28.42	B	C
ATOM	2865	CG	PHE	B	227	5.401	39.718	42.453	1.00	27.26	B	C
ATOM	2866	CD1	PHE	B	227	4.880	40.346	41.321	1.00	27.70	B	C
ATOM	2867	CD2	PHE	B	227	6.352	38.712	42.286	1.00	27.41	B	C
ATOM	2868	CE1	PHE	B	227	5.308	39.976	40.041	1.00	27.47	B	C
ATOM	2869	CE2	PHE	B	227	6.786	38.334	41.011	1.00	27.41	B	C
ATOM	2870	CZ	PHE	B	227	6.261	38.969	39.887	1.00	27.84	B	C
ATOM	2871	C	PHE	B	227	4.453	41.850	45.525	1.00	26.66	B	C
ATOM	2872	O	PHE	B	227	5.372	42.385	46.229	1.00	25.45	B	O
ATOM	2873	N	ASP	B	228	3.273	41.442	45.983	1.00	24.91	B	N
ATOM	2874	CA	ASP	B	228	2.870	41.576	47.375	1.00	25.21	B	C
ATOM	2875	CB	ASP	B	228	1.346	41.623	47.484	1.00	25.97	B	C
ATOM	2876	CG	ASP	B	228	0.675	40.479	46.742	1.00	26.97	B	C
ATOM	2877	OD1	ASP	B	228	0.468	40.611	45.525	1.00	33.21	B	O
ATOM	2878	OD2	ASP	B	228	0.373	39.440	47.359	1.00	27.04	B	O
ATOM	2879	C	ASP	B	228	3.394	40.357	48.129	1.00	26.47	B	C
ATOM	2880	O	ASP	B	228	3.979	39.447	47.528	1.00	26.50	B	O
ATOM	2881	N	GLU	B	229	3.158	40.327	49.436	1.00	25.93	B	N
ATOM	2882	CA	GLU	B	229	3.627	39.234	50.275	1.00	25.05	B	C
ATOM	2883	CB	GLU	B	229	3.425	39.579	51.757	1.00	26.99	B	C
ATOM	2884	CG	GLU	B	229	4.230	40.789	52.233	1.00	30.82	B	C
ATOM	2885	CD	GLU	B	229	4.296	40.905	53.753	1.00	31.53	B	C
ATOM	2886	OE1	GLU	B	229	3.239	41.053	54.403	1.00	32.47	B	O
ATOM	2887	OE2	GLU	B	229	5.415	40.847	54.299	1.00	33.80	B	O
ATOM	2888	C	GLU	B	229	2.961	37.900	49.973	1.00	25.00	B	C
ATOM	2889	O	GLU	B	229	3.624	36.855	49.985	1.00	22.64	B	O
ATOM	2890	N	GLN	B	230	1.657	37.930	49.702	1.00	23.27	B	N
ATOM	2891	CA	GLN	B	230	0.925	36.698	49.420	1.00	25.73	B	C
ATOM	2892	CB	GLN	B	230	-0.577	36.990	49.254	1.00	30.97	B	C
ATOM	2893	CG	GLN	B	230	-1.443	35.736	49.099	1.00	37.32	B	C
ATOM	2894	CD	GLN	B	230	-2.902	36.043	48.773	1.00	41.26	B	C

	ATOM	2895	OE1	GLN	B	230	-3.214	36.601	47.720	1.00	43.42	B	O
	ATOM	2896	NE2	GLN	B	230	-3.800	35.673	49.679	1.00	43.12	B	N
	ATOM	2897	C	GLN	B	230	1.477	36.003	48.173	1.00	22.96	B	C
	ATOM	2898	O	GLN	B	230	1.779	34.811	48.203	1.00	22.41	B	O
5	ATOM	2899	N	ARG	B	231	1.618	36.750	47.081	1.00	21.69	B	N
	ATOM	2900	CA	ARG	B	231	2.151	36.196	45.841	1.00	20.70	B	C
	ATOM	2901	CB	ARG	B	231	2.067	37.237	44.720	1.00	24.11	B	C
	ATOM	2902	CG	ARG	B	231	2.972	36.943	43.534	1.00	29.60	B	C
	ATOM	2903	CD	ARG	B	231	2.207	36.654	42.261	1.00	32.47	B	C
10	ATOM	2904	NE	ARG	B	231	1.381	37.776	41.827	1.00	35.86	B	N
	ATOM	2905	CZ	ARG	B	231	1.031	37.992	40.562	1.00	38.81	B	C
	ATOM	2906	NH1	ARG	B	231	0.269	39.031	40.249	1.00	39.91	B	N
	ATOM	2907	NH2	ARG	B	231	1.466	37.183	39.602	1.00	38.33	B	N
	ATOM	2908	C	ARG	B	231	3.606	35.719	46.001	1.00	19.50	B	C
15	ATOM	2909	O	ARG	B	231	3.957	34.622	45.557	1.00	17.71	B	O
	ATOM	2910	N	THR	B	232	4.441	36.538	46.635	1.00	17.49	B	N
	ATOM	2911	CA	THR	B	232	5.838	36.184	46.847	1.00	16.16	B	C
	ATOM	2912	CB	THR	B	232	6.612	37.312	47.576	1.00	19.54	B	C
	ATOM	2913	OG1	THR	B	232	6.597	38.504	46.782	1.00	13.78	B	O
20	ATOM	2914	CG2	THR	B	232	8.082	36.879	47.834	1.00	14.78	B	C
	ATOM	2915	C	THR	B	232	5.956	34.904	47.682	1.00	17.18	B	C
	ATOM	2916	O	THR	B	232	6.672	33.984	47.307	1.00	15.09	B	O
	ATOM	2917	N	ALA	B	233	5.243	34.852	48.807	1.00	19.12	B	N
	ATOM	2918	CA	ALA	B	233	5.264	33.684	49.695	1.00	18.94	B	C
25	ATOM	2919	CB	ALA	B	233	4.352	33.925	50.906	1.00	17.71	B	C
	ATOM	2920	C	ALA	B	233	4.828	32.407	48.966	1.00	19.02	B	C
	ATOM	2921	O	ALA	B	233	5.417	31.334	49.157	1.00	18.32	B	O
	ATOM	2922	N	THR	B	234	3.785	32.527	48.148	1.00	19.42	B	N
30	ATOM	2923	CA	THR	B	234	3.275	31.399	47.370	1.00	18.40	B	C
	ATOM	2924	CB	THR	B	234	1.975	31.784	46.620	1.00	17.88	B	C
	ATOM	2925	OG1	THR	B	234	0.965	32.134	47.575	1.00	15.16	B	O
	ATOM	2926	CG2	THR	B	234	1.480	30.618	45.762	1.00	16.22	B	C
	ATOM	2927	C	THR	B	234	4.329	30.932	46.364	1.00	18.28	B	C
	ATOM	2928	O	THR	B	234	4.550	29.735	46.196	1.00	20.75	B	O
35	ATOM	2929	N	TYR	B	235	4.981	31.876	45.694	1.00	19.08	B	N
	ATOM	2930	CA	TYR	B	235	6.034	31.540	44.736	1.00	18.92	B	C
	ATOM	2931	CB	TYR	B	235	6.514	32.803	44.014	1.00	19.29	B	C
	ATOM	2932	CG	TYR	B	235	5.661	33.258	42.851	1.00	21.57	B	C
	ATOM	2933	CD1	TYR	B	235	4.389	32.729	42.634	1.00	23.85	B	C
40	ATOM	2934	CE1	TYR	B	235	3.589	33.176	41.579	1.00	24.93	B	C
	ATOM	2935	CD2	TYR	B	235	6.116	34.247	41.984	1.00	21.08	B	C
	ATOM	2936	CE2	TYR	B	235	5.335	34.705	40.926	1.00	24.94	B	C
	ATOM	2937	CZ	TYR	B	235	4.063	34.168	40.728	1.00	26.16	B	C
	ATOM	2938	OH	TYR	B	235	3.267	34.628	39.695	1.00	22.88	B	O
45	ATOM	2939	C	TYR	B	235	7.242	30.871	45.423	1.00	18.91	B	C
	ATOM	2940	O	TYR	B	235	7.855	29.956	44.869	1.00	18.47	B	O
	ATOM	2941	N	ILE	B	236	7.603	31.336	46.619	1.00	18.40	B	N
	ATOM	2942	CA	ILE	B	236	8.745	30.741	47.321	1.00	17.73	B	C
	ATOM	2943	CB	ILE	B	236	9.188	31.601	48.541	1.00	18.76	B	C
50	ATOM	2944	CG2	ILE	B	236	10.387	30.945	49.254	1.00	18.52	B	C
	ATOM	2945	CG1	ILE	B	236	9.612	32.999	48.065	1.00	19.28	B	C
	ATOM	2946	CD1	ILE	B	236	10.744	32.987	47.035	1.00	16.65	B	C
	ATOM	2947	C	ILE	B	236	8.407	29.322	47.781	1.00	16.37	B	C
	ATOM	2948	O	ILE	B	236	9.274	28.460	47.824	1.00	15.52	B	O
55	ATOM	2949	N	THR	B	237	7.138	29.086	48.109	1.00	17.75	B	N
	ATOM	2950	CA	THR	B	237	6.685	27.770	48.545	1.00	18.73	B	C
	ATOM	2951	CB	THR	B	237	5.203	27.813	49.028	1.00	20.81	B	C
	ATOM	2952	OG1	THR	B	237	5.124	28.585	50.224	1.00	20.67	B	O
	ATOM	2953	CG2	THR	B	237	4.677	26.420	49.334	1.00	20.82	B	C
60	ATOM	2954	C	THR	B	237	6.818	26.764	47.410	1.00	18.80	B	C
	ATOM	2955	O	THR	B	237	7.425	25.710	47.576	1.00	20.21	B	O
	ATOM	2956	N	GLU	B	238	6.253	27.092	46.252	1.00	20.60	B	N
	ATOM	2957	CA	GLU	B	238	6.320	26.199	45.099	1.00	19.19	B	C
	ATOM	2958	CB	GLU	B	238	5.555	26.813	43.918	1.00	20.66	B	C
65	ATOM	2959	CG	GLU	B	238	4.036	26.779	44.100	1.00	23.37	B	C
	ATOM	2960	CD	GLU	B	238	3.313	27.786	43.224	1.00	24.80	B	C
	ATOM	2961	OE1	GLU	B	238	3.581	27.842	42.009	1.00	25.78	B	O
	ATOM	2962	OE2	GLU	B	238	2.466	28.527	43.755	1.00	28.41	B	O
	ATOM	2963	C	GLU	B	238	7.767	25.917	44.705	1.00	19.31	B	C
70	ATOM	2964	O	GLU	B	238	8.126	24.780	44.361	1.00	17.16	B	O
	ATOM	2965	N	LEU	B	239	8.598	26.954	44.751	1.00	18.37	B	N
	ATOM	2966	CA	LEU	B	239	10.004	26.801	44.401	1.00	17.98	B	C

ATOM	2967	CB	LEU	B	239	10.690	28.166	44.357	1.00	19.30	B	C
ATOM	2968	CG	LEU	B	239	10.569	28.862	43.002	1.00	22.62	B	C
ATOM	2969	CD1	LEU	B	239	10.915	30.346	43.126	1.00	23.53	B	C
ATOM	2970	CD2	LEU	B	239	11.493	28.157	42.008	1.00	23.78	B	C
ATOM	2971	C	LEU	B	239	10.746	25.877	45.362	1.00	18.38	B	C
ATOM	2972	O	LEU	B	239	11.517	25.025	44.926	1.00	18.06	B	O
ATOM	2973	N	ALA	B	240	10.514	26.047	46.665	1.00	16.60	B	N
ATOM	2974	CA	ALA	B	240	11.180	25.214	47.668	1.00	17.68	B	C
ATOM	2975	CB	ALA	B	240	10.830	25.701	49.080	1.00	16.34	B	C
ATOM	2976	C	ALA	B	240	10.777	23.750	47.496	1.00	18.39	B	C
ATOM	2977	O	ALA	B	240	11.606	22.856	47.641	1.00	16.04	B	O
ATOM	2978	N	ASN	B	241	9.502	23.518	47.179	1.00	19.07	B	N
ATOM	2979	CA	ASN	B	241	9.009	22.166	46.967	1.00	21.46	B	C
ATOM	2980	CB	ASN	B	241	7.517	22.167	46.602	1.00	23.76	B	C
ATOM	2981	CG	ASN	B	241	6.625	22.096	47.814	1.00	28.59	B	C
ATOM	2982	OD1	ASN	B	241	6.917	21.367	48.759	1.00	31.92	B	O
ATOM	2983	ND2	ASN	B	241	5.524	22.842	47.794	1.00	29.40	B	N
ATOM	2984	C	ASN	B	241	9.789	21.536	45.833	1.00	21.94	B	C
ATOM	2985	O	ASN	B	241	10.282	20.408	45.951	1.00	23.36	B	O
ATOM	2986	N	ALA	B	242	9.898	22.279	44.735	1.00	20.78	B	N
ATOM	2987	CA	ALA	B	242	10.614	21.816	43.553	1.00	21.85	B	C
ATOM	2988	CB	ALA	B	242	10.437	22.818	42.426	1.00	18.99	B	C
ATOM	2989	C	ALA	B	242	12.105	21.567	43.820	1.00	21.42	B	C
ATOM	2990	O	ALA	B	242	12.634	20.508	43.488	1.00	21.59	B	O
ATOM	2991	N	LEU	B	243	12.782	22.537	44.426	1.00	22.94	B	N
ATOM	2992	CA	LEU	B	243	14.209	22.383	44.730	1.00	21.96	B	C
ATOM	2993	CB	LEU	B	243	14.751	23.669	45.360	1.00	19.53	B	C
ATOM	2994	CG	LEU	B	243	14.744	24.896	44.439	1.00	20.66	B	C
ATOM	2995	CD1	LEU	B	243	15.174	26.127	45.213	1.00	20.26	B	C
ATOM	2996	CD2	LEU	B	243	15.674	24.656	43.266	1.00	20.88	B	C
ATOM	2997	C	LEU	B	243	14.457	21.196	45.668	1.00	21.93	B	C
ATOM	2998	O	LEU	B	243	15.449	20.469	45.535	1.00	20.07	B	O
ATOM	2999	N	SER	B	244	13.558	21.014	46.626	1.00	22.84	B	N
ATOM	3000	CA	SER	B	244	13.676	19.913	47.572	1.00	25.72	B	C
ATOM	3001	CB	SER	B	244	12.528	19.966	48.582	1.00	26.38	B	C
ATOM	3002	OG	SER	B	244	12.707	18.992	49.589	1.00	31.74	B	O
ATOM	3003	C	SER	B	244	13.646	18.594	46.800	1.00	26.65	B	C
ATOM	3004	O	SER	B	244	14.497	17.725	47.001	1.00	28.75	B	O
ATOM	3005	N	TYR	B	245	12.667	18.450	45.912	1.00	25.41	B	N
ATOM	3006	CA	TYR	B	245	12.534	17.246	45.101	1.00	26.59	B	C
ATOM	3007	CB	TYR	B	245	11.297	17.347	44.210	1.00	28.10	B	C
ATOM	3008	CG	TYR	B	245	11.234	16.369	43.050	1.00	29.48	B	C
ATOM	3009	CD1	TYR	B	245	11.789	16.695	41.808	1.00	27.01	B	C
ATOM	3010	CE1	TYR	B	245	11.746	15.806	40.740	1.00	25.91	B	C
ATOM	3011	CD2	TYR	B	245	10.625	15.113	43.193	1.00	29.43	B	C
ATOM	3012	CE2	TYR	B	245	10.576	14.210	42.124	1.00	29.19	B	C
ATOM	3013	CZ	TYR	B	245	11.144	14.568	40.900	1.00	27.94	B	C
ATOM	3014	OH	TYR	B	245	11.131	13.687	39.842	1.00	26.95	B	O
ATOM	3015	C	TYR	B	245	13.808	17.026	44.261	1.00	27.59	B	C
ATOM	3016	O	TYR	B	245	14.272	15.897	44.117	1.00	27.11	B	O
ATOM	3017	N	CYS	B	246	14.372	18.099	43.711	1.00	27.30	B	N
ATOM	3018	CA	CYS	B	246	15.586	17.965	42.907	1.00	27.67	B	C
ATOM	3019	CB	CYS	B	246	15.926	19.284	42.202	1.00	27.42	B	C
ATOM	3020	SG	CYS	B	246	14.898	19.706	40.755	1.00	29.37	B	S
ATOM	3021	C	CYS	B	246	16.787	17.518	43.753	1.00	26.99	B	C
ATOM	3022	O	CYS	B	246	17.568	16.670	43.333	1.00	24.30	B	O
ATOM	3023	N	HIS	B	247	16.938	18.097	44.940	1.00	27.86	B	N
ATOM	3024	CA	HIS	B	247	18.048	17.734	45.813	1.00	28.63	B	C
ATOM	3025	CB	HIS	B	247	18.007	18.546	47.116	1.00	27.63	B	C
ATOM	3026	CG	HIS	B	247	18.519	19.950	46.976	1.00	27.06	B	C
ATOM	3027	CD2	HIS	B	247	18.746	20.716	45.882	1.00	26.78	B	C
ATOM	3028	ND1	HIS	B	247	18.873	20.724	48.062	1.00	26.58	B	N
ATOM	3029	CE1	HIS	B	247	19.299	21.902	47.643	1.00	24.28	B	C
ATOM	3030	NE2	HIS	B	247	19.232	21.923	46.325	1.00	24.21	B	N
ATOM	3031	C	HIS	B	247	18.006	16.241	46.128	1.00	30.30	B	C
ATOM	3032	O	HIS	B	247	19.046	15.594	46.243	1.00	29.75	B	O
ATOM	3033	N	SER	B	248	16.801	15.691	46.245	1.00	31.77	B	N
ATOM	3034	CA	SER	B	248	16.641	14.275	46.550	1.00	34.48	B	C
ATOM	3035	CB	SER	B	248	15.169	13.943	46.824	1.00	34.54	B	C
ATOM	3036	OG	SER	B	248	14.419	13.874	45.621	1.00	34.42	B	O
ATOM	3037	C	SER	B	248	17.166	13.396	45.417	1.00	36.24	B	C
ATOM	3038	O	SER	B	248	17.527	12.239	45.640	1.00	39.13	B	O

	ATOM	3039	N	LYS	B	249	17.206	13.937	44.205	1.00	37.49	B N
	ATOM	3040	CA	LYS	B	249	17.714	13.183	43.065	1.00	38.33	B C
	ATOM	3041	CB	LYS	B	249	16.752	13.291	41.882	1.00	39.56	B C
	ATOM	3042	CG	LYS	B	249	15.480	12.470	42.075	1.00	41.09	B C
5	ATOM	3043	CD	LYS	B	249	14.692	12.348	40.783	1.00	42.87	B C
	ATOM	3044	CE	LYS	B	249	13.544	11.345	40.903	1.00	44.69	B C
	ATOM	3045	NZ	LYS	B	249	14.008	9.940	41.115	1.00	43.80	B N
	ATOM	3046	C	LYS	B	249	19.130	13.649	42.667	1.00	38.25	B C
	ATOM	3047	O	LYS	B	249	19.535	13.500	41.520	1.00	38.18	B O
10	ATOM	3048	N	ALA	B	250	19.823	14.208	43.639	1.00	38.25	B N
	ATOM	3049	CA	ALA	B	250	21.180	14.693	43.429	1.00	38.88	B C
	ATOM	3050	CB	ALA	B	250	22.128	13.506	43.260	1.00	37.35	B C
	ATOM	3051	C	ALA	B	250	21.294	15.642	42.234	1.00	39.66	B C
	ATOM	3052	O	ALA	B	250	22.256	15.586	41.469	1.00	39.73	B O
15	ATOM	3053	N	VAL	B	251	20.312	16.521	42.077	1.00	40.68	B N
	ATOM	3054	CA	VAL	B	251	20.331	17.475	40.976	1.00	41.44	B C
	ATOM	3055	CB	VAL	B	251	19.009	17.448	40.197	1.00	39.71	B C
	ATOM	3056	CG1	VAL	B	251	18.996	18.543	39.156	1.00	36.93	B C
	ATOM	3057	CG2	VAL	B	251	18.833	16.099	39.542	1.00	39.66	B C
20	ATOM	3058	C	VAL	B	251	20.575	18.887	41.487	1.00	43.36	B C
	ATOM	3059	O	VAL	B	251	19.857	19.361	42.361	1.00	43.18	B O
	ATOM	3060	N	ALA	B	252	21.594	19.572	41.411	1.00	47.23	B N
	ATOM	3061	CA	ALA	B	252	21.800	20.930	41.937	1.00	51.57	B C
	ATOM	3062	CB	ALA	B	252	23.072	20.979	42.781	1.00	50.06	B C
25	ATOM	3063	C	ALA	B	252	21.867	21.974	40.811	1.00	55.17	B C
	ATOM	3064	O	ALA	B	252	22.516	21.755	39.786	1.00	55.31	B O
	ATOM	3065	N	HIS	B	253	21.201	23.110	41.025	1.00	59.25	B N
	ATOM	3066	CA	HIS	B	253	21.127	24.196	40.039	1.00	62.40	B C
	ATOM	3067	CB	HIS	B	253	19.928	25.100	40.346	1.00	63.38	B C
30	ATOM	3068	CG	HIS	B	253	18.626	24.569	39.838	1.00	65.58	B C
	ATOM	3069	CD2	HIS	B	253	17.728	25.093	38.970	1.00	65.78	B C
	ATOM	3070	ND1	HIS	B	253	18.131	23.335	40.205	1.00	66.21	B N
	ATOM	3071	CE1	HIS	B	253	16.985	23.122	39.583	1.00	66.24	B C
	ATOM	3072	NE2	HIS	B	253	16.718	24.173	38.828	1.00	66.35	B N
35	ATOM	3073	C	HIS	B	253	22.343	25.091	39.812	1.00	64.23	B C
	ATOM	3074	O	HIS	B	253	23.157	24.827	38.924	1.00	64.24	B O
	ATOM	3075	N	ARG	B	254	22.431	26.162	40.603	1.00	66.29	B N
	ATOM	3076	CA	ARG	B	254	23.501	27.162	40.503	1.00	67.93	B C
	ATOM	3077	CB	ARG	B	254	24.829	26.507	40.106	1.00	69.34	B C
40	ATOM	3078	CG	ARG	B	254	25.429	25.629	41.199	1.00	72.18	B C
	ATOM	3079	CD	ARG	B	254	26.435	24.626	40.649	1.00	73.87	B C
	ATOM	3080	NE	ARG	B	254	27.423	25.232	39.760	1.00	76.14	B N
	ATOM	3081	CZ	ARG	B	254	28.423	24.559	39.197	1.00	77.32	B C
	ATOM	3082	NH1	ARG	B	254	28.566	23.259	39.435	1.00	77.53	B N
45	ATOM	3083	NH2	ARG	B	254	29.275	25.180	38.391	1.00	77.47	B N
	ATOM	3084	C	ARG	B	254	23.093	28.203	39.455	1.00	68.10	B C
	ATOM	3085	O	ARG	B	254	23.941	28.818	38.805	1.00	68.48	B O
	ATOM	3086	N	ASP	B	255	21.779	28.383	39.311	1.00	67.94	B N
	ATOM	3087	CA	ASP	B	255	21.181	29.321	38.358	1.00	66.09	B C
50	ATOM	3088	CB	ASP	B	255	21.768	29.117	36.960	1.00	68.18	B C
	ATOM	3089	CG	ASP	B	255	20.978	29.848	35.891	1.00	70.20	B C
	ATOM	3090	OD1	ASP	B	255	20.977	31.098	35.906	1.00	70.85	B O
	ATOM	3091	OD2	ASP	B	255	20.346	29.176	35.045	1.00	70.61	B O
	ATOM	3092	C	ASP	B	255	19.670	29.086	38.290	1.00	64.02	B C
55	ATOM	3093	O	ASP	B	255	19.224	27.980	37.966	1.00	63.85	B O
	ATOM	3094	N	ILE	B	256	18.887	30.123	38.587	1.00	60.24	B N
	ATOM	3095	CA	ILE	B	256	17.432	30.007	38.557	1.00	56.06	B C
	ATOM	3096	CB	ILE	B	256	16.938	29.251	39.813	1.00	56.48	B C
	ATOM	3097	CG2	ILE	B	256	17.097	30.123	41.051	1.00	57.30	B C
60	ATOM	3098	CG1	ILE	B	256	15.483	28.833	39.637	1.00	56.77	B C
	ATOM	3099	CD1	ILE	B	256	15.012	27.833	40.671	1.00	57.42	B C
	ATOM	3100	C	ILE	B	256	16.727	31.371	38.444	1.00	52.46	B C
	ATOM	3101	O	ILE	B	256	15.769	31.661	39.154	1.00	51.61	B O
	ATOM	3102	N	LYS	B	257	17.209	32.193	37.521	1.00	48.41	B N
65	ATOM	3103	CA	LYS	B	257	16.684	33.536	37.258	1.00	44.89	B C
	ATOM	3104	CB	LYS	B	257	17.469	34.142	36.094	1.00	45.52	B C
	ATOM	3105	CG	LYS	B	257	18.981	34.051	36.249	1.00	48.52	B C
	ATOM	3106	CD	LYS	B	257	19.703	34.586	35.017	1.00	50.54	B C
	ATOM	3107	CE	LYS	B	257	19.499	33.695	33.791	1.00	50.70	B C
70	ATOM	3108	NZ	LYS	B	257	20.251	32.406	33.875	1.00	51.10	B N
	ATOM	3109	C	LYS	B	257	15.177	33.614	36.941	1.00	40.75	B C
	ATOM	3110	O	LYS	B	257	14.548	32.614	36.614	1.00	40.52	B O

ATOM	3111	N	PRO	B	258	14.480	34.397	36.931	1.00	37.08	B	N
ATOM	3112	CD	PRO	B	258	15.445	35.391	37.431	1.00	36.34	B	C
ATOM	3113	CA	PRO	B	258	13.167	35.015	36.690	1.00	35.17	B	C
ATOM	3114	CB	PRO	B	258	13.397	36.489	37.038	1.00	34.26	B	C
ATOM	3115	CG	PRO	B	258	14.544	36.448	38.017	1.00	33.40	B	C
ATOM	3116	C	PRO	B	258	12.770	34.825	35.227	1.00	34.61	B	C
ATOM	3117	O	PRO	B	258	11.604	34.576	34.908	1.00	31.39	B	O
ATOM	3118	N	GLU	B	259	13.757	34.954	34.346	1.00	33.54	B	N
ATOM	3119	CA	GLU	B	259	13.540	34.769	32.918	1.00	34.62	B	C
ATOM	3120	CB	GLU	B	259	14.706	35.332	32.100	1.00	37.22	B	C
ATOM	3121	CG	GLU	B	259	15.143	36.745	32.442	1.00	41.67	B	C
ATOM	3122	CD	GLU	B	259	15.934	36.826	33.735	1.00	44.39	B	C
ATOM	3123	OE1	GLU	B	259	16.564	37.874	33.978	1.00	46.55	B	O
ATOM	3124	OE2	GLU	B	259	15.924	35.851	34.515	1.00	46.90	B	O
ATOM	3125	C	GLU	B	259	13.469	33.265	32.678	1.00	34.06	B	C
ATOM	3126	O	GLU	B	259	13.004	32.812	31.632	1.00	34.68	B	O
ATOM	3127	N	ASN	B	260	13.943	32.492	33.652	1.00	31.75	B	N
ATOM	3128	CA	ASN	B	260	13.941	31.042	33.527	1.00	30.54	B	C
ATOM	3129	CB	ASN	B	260	15.262	30.455	34.035	1.00	34.15	B	C
ATOM	3130	CG	ASN	B	260	16.474	31.178	33.478	1.00	39.70	B	C
ATOM	3131	OD1	ASN	B	260	16.454	31.681	32.347	1.00	41.30	B	O
ATOM	3132	ND2	ASN	B	260	17.545	31.226	34.265	1.00	40.33	B	N
ATOM	3133	C	ASN	B	260	12.785	30.413	34.284	1.00	27.70	B	C
ATOM	3134	O	ASN	B	260	12.723	29.194	34.423	1.00	28.09	B	O
ATOM	3135	N	LEU	B	261	11.879	31.244	34.783	1.00	23.87	B	N
ATOM	3136	CA	LEU	B	261	10.715	30.748	35.511	1.00	23.63	B	C
ATOM	3137	CB	LEU	B	261	10.636	31.393	36.904	1.00	23.52	B	C
ATOM	3138	CG	LEU	B	261	11.859	31.157	37.802	1.00	23.80	B	C
ATOM	3139	CD1	LEU	B	261	11.784	32.065	39.013	1.00	23.16	B	C
ATOM	3140	CD2	LEU	B	261	11.918	29.696	38.233	1.00	23.15	B	C
ATOM	3141	C	LEU	B	261	9.486	31.094	34.683	1.00	22.79	B	C
ATOM	3142	O	LEU	B	261	9.248	32.259	34.360	1.00	23.35	B	O
ATOM	3143	N	LEU	B	262	8.720	30.072	34.329	1.00	21.85	B	N
ATOM	3144	CA	LEU	B	262	7.530	30.240	33.503	1.00	20.81	B	C
ATOM	3145	CB	LEU	B	262	7.583	29.241	32.338	1.00	18.28	B	C
ATOM	3146	CG	LEU	B	262	8.805	29.444	31.427	1.00	20.74	B	C
ATOM	3147	CD1	LEU	B	262	9.022	28.247	30.528	1.00	17.18	B	C
ATOM	3148	CD2	LEU	B	262	8.594	30.704	30.600	1.00	23.22	B	C
ATOM	3149	C	LEU	B	262	6.260	30.050	34.324	1.00	20.95	B	C
ATOM	3150	O	LEU	B	262	6.320	29.607	35.468	1.00	21.65	B	O
ATOM	3151	N	LEU	B	263	5.118	30.385	33.731	1.00	20.04	B	N
ATOM	3152	CA	LEU	B	263	3.818	30.291	34.401	1.00	19.89	B	C
ATOM	3153	CB	LEU	B	263	3.199	31.682	34.542	1.00	19.96	B	C
ATOM	3154	CG	LEU	B	263	3.895	32.673	35.485	1.00	22.61	B	C
ATOM	3155	CD1	LEU	B	263	3.332	34.074	35.269	1.00	19.88	B	C
ATOM	3156	CD2	LEU	B	263	3.689	32.218	36.938	1.00	19.42	B	C
ATOM	3157	C	LEU	B	263	2.828	29.405	33.667	1.00	20.69	B	C
ATOM	3158	O	LEU	B	263	2.555	29.607	32.477	1.00	19.05	B	O
ATOM	3159	N	GLY	B	264	2.285	28.434	34.390	1.00	20.39	B	N
ATOM	3160	CA	GLY	B	264	1.318	27.531	33.810	1.00	22.81	B	C
ATOM	3161	C	GLY	B	264	-0.058	28.166	33.723	1.00	23.93	B	C
ATOM	3162	O	GLY	B	264	-0.267	29.307	34.146	1.00	23.55	B	O
ATOM	3163	N	SER	B	265	-0.996	27.406	33.178	1.00	26.43	B	N
ATOM	3164	CA	SER	B	265	-2.375	27.846	33.002	1.00	29.74	B	C
ATOM	3165	CB	SER	B	265	-3.224	26.687	32.478	1.00	30.89	B	C
ATOM	3166	OG	SER	B	265	-4.593	27.054	32.458	1.00	37.32	B	O
ATOM	3167	C	SER	B	265	-3.026	28.398	34.267	1.00	30.10	B	C
ATOM	3168	O	SER	B	265	-3.786	29.356	34.203	1.00	31.27	B	O
ATOM	3169	N	ALA	B	266	-2.738	27.790	35.411	1.00	29.46	B	N
ATOM	3170	CA	ALA	B	266	-3.319	28.239	36.670	1.00	28.49	B	C
ATOM	3171	CB	ALA	B	266	-3.645	27.040	37.546	1.00	27.90	B	C
ATOM	3172	C	ALA	B	266	-2.424	29.202	37.433	1.00	27.49	B	C
ATOM	3173	O	ALA	B	266	-2.673	29.486	38.594	1.00	26.71	B	O
ATOM	3174	N	GLY	B	267	-1.380	29.704	36.785	1.00	28.52	B	N
ATOM	3175	CA	GLY	B	267	-0.485	30.630	37.458	1.00	27.29	B	C
ATOM	3176	C	GLY	B	267	0.556	29.951	38.335	1.00	26.61	B	C
ATOM	3177	O	GLY	B	267	1.155	30.591	39.203	1.00	27.45	B	O
ATOM	3178	N	GLU	B	268	0.780	28.660	38.117	1.00	25.29	B	N
ATOM	3179	CA	GLU	B	268	1.766	27.924	38.905	1.00	26.30	B	C
ATOM	3180	CB	GLU	B	268	1.409	26.433	38.967	1.00	27.43	B	C
ATOM	3181	CG	GLU	B	268	0.012	26.107	38.488	1.00	34.47	B	C
ATOM	3182	CD	GLU	B	268	-0.087	26.008	36.976	1.00	35.53	B	C

ATOM	3183	OE1	GLU	B	268	0.297	24.958	36.423	1.00	38.92	B	O
ATOM	3184	OE2	GLU	B	268	-0.546	26.979	36.339	1.00	38.49	B	O
ATOM	3185	C	GLU	B	268	3.154	28.083	38.287	1.00	24.38	B	C
ATOM	3186	O	GLU	B	268	3.300	28.062	37.063	1.00	21.68	B	O
ATOM	3187	N	LEU	B	269	4.171	28.250	39.129	1.00	23.82	B	N
ATOM	3188	CA	LEU	B	269	5.542	28.398	38.634	1.00	21.61	B	C
ATOM	3189	CB	LEU	B	269	6.492	28.808	39.761	1.00	24.33	B	C
ATOM	3190	CG	LEU	B	269	6.545	30.246	40.265	1.00	25.70	B	C
ATOM	3191	CD1	LEU	B	269	7.693	30.382	41.252	1.00	24.92	B	C
ATOM	3192	CD2	LEU	B	269	6.751	31.198	39.103	1.00	27.39	B	C
ATOM	3193	C	LEU	B	269	6.061	27.099	38.034	1.00	19.77	B	C
ATOM	3194	O	LEU	B	269	5.703	26.015	38.485	1.00	19.34	B	O
ATOM	3195	N	LYS	B	270	6.909	27.222	37.017	1.00	19.92	B	N
ATOM	3196	CA	LYS	B	270	7.525	26.074	36.356	1.00	20.30	B	C
ATOM	3197	CB	LYS	B	270	6.902	25.836	34.972	1.00	18.33	B	C
ATOM	3198	CG	LYS	B	270	5.393	25.615	34.964	1.00	18.74	B	C
ATOM	3199	CD	LYS	B	270	5.012	24.155	35.137	1.00	15.50	B	C
ATOM	3200	CE	LYS	B	270	3.491	23.994	35.128	1.00	18.10	B	C
ATOM	3201	NZ	LYS	B	270	3.046	22.575	35.077	1.00	15.24	B	N
ATOM	3202	C	LYS	B	270	9.019	26.383	36.178	1.00	20.49	B	C
ATOM	3203	O	LYS	B	270	9.373	27.374	35.550	1.00	18.08	B	O
ATOM	3204	N	ILE	B	271	9.889	25.545	36.737	1.00	21.09	B	N
ATOM	3205	CA	ILE	B	271	11.329	25.756	36.587	1.00	20.68	B	C
ATOM	3206	CB	ILE	B	271	12.133	25.016	37.674	1.00	21.21	B	C
ATOM	3207	CG2	ILE	B	271	13.640	25.176	37.413	1.00	19.34	B	C
ATOM	3208	CG1	ILE	B	271	11.761	25.553	39.060	1.00	23.24	B	C
ATOM	3209	CD1	ILE	B	271	12.514	24.863	40.210	1.00	24.09	B	C
ATOM	3210	C	ILE	B	271	11.754	25.207	35.224	1.00	20.59	B	C
ATOM	3211	O	ILE	B	271	11.482	24.051	34.911	1.00	19.44	B	O
ATOM	3212	N	ALA	B	272	12.410	26.034	34.416	1.00	19.34	B	N
ATOM	3213	CA	ALA	B	272	12.858	25.598	33.095	1.00	24.16	B	C
ATOM	3214	CB	ALA	B	272	12.404	26.594	32.037	1.00	20.99	B	C
ATOM	3215	C	ALA	B	272	14.384	25.434	33.039	1.00	26.77	B	C
ATOM	3216	O	ALA	B	272	15.106	26.155	33.723	1.00	27.46	B	O
ATOM	3217	N	ASP	B	273	14.843	24.478	32.225	1.00	29.94	B	N
ATOM	3218	CA	ASP	B	273	16.265	24.150	32.014	1.00	32.45	B	C
ATOM	3219	CB	ASP	B	273	17.153	25.351	32.319	1.00	33.94	B	C
ATOM	3220	CG	ASP	B	273	17.622	26.038	31.068	1.00	38.34	B	C
ATOM	3221	OD1	ASP	B	273	18.171	27.165	31.162	1.00	41.51	B	O
ATOM	3222	OD2	ASP	B	273	17.438	25.436	29.986	1.00	36.50	B	O
ATOM	3223	C	ASP	B	273	16.799	22.930	32.767	1.00	34.27	B	C
ATOM	3224	O	ASP	B	273	17.928	22.472	32.518	1.00	34.48	B	O
ATOM	3225	N	GLY	B	290	22.452	32.822	36.840	1.00	57.41	B	N
ATOM	3226	CA	GLY	B	290	22.919	33.188	35.513	1.00	56.55	B	C
ATOM	3227	C	GLY	B	290	23.992	34.260	35.563	1.00	56.09	B	C
ATOM	3228	O	GLY	B	290	25.185	33.954	35.650	1.00	56.35	B	O
ATOM	3229	N	THR	B	291	23.572	35.522	35.508	1.00	54.56	B	N
ATOM	3230	CA	THR	B	291	24.511	36.633	35.555	1.00	52.44	B	C
ATOM	3231	CB	THR	B	291	23.813	37.967	35.195	1.00	53.95	B	C
ATOM	3232	OG1	THR	B	291	22.687	38.172	36.056	1.00	54.88	B	O
ATOM	3233	CG2	THR	B	291	23.338	37.946	33.746	1.00	55.03	B	C
ATOM	3234	C	THR	B	291	25.140	36.738	36.945	1.00	50.11	B	C
ATOM	3235	O	THR	B	291	24.840	35.940	37.840	1.00	47.96	B	O
ATOM	3236	N	LEU	B	292	26.010	37.727	37.123	1.00	47.85	B	N
ATOM	3237	CA	LEU	B	292	26.695	37.926	38.395	1.00	46.13	B	C
ATOM	3238	CB	LEU	B	292	27.664	39.109	38.280	1.00	46.70	B	C
ATOM	3239	CG	LEU	B	292	28.706	39.250	39.393	1.00	47.14	B	C
ATOM	3240	CD1	LEU	B	292	29.422	37.921	39.596	1.00	46.68	B	C
ATOM	3241	CD2	LEU	B	292	29.704	40.342	39.030	1.00	46.77	B	C
ATOM	3242	C	LEU	B	292	25.740	38.143	39.573	1.00	44.02	B	C
ATOM	3243	O	LEU	B	292	25.967	37.638	40.675	1.00	43.84	B	O
ATOM	3244	N	ASP	B	293	24.663	38.879	39.330	1.00	41.14	B	N
ATOM	3245	CA	ASP	B	293	23.687	39.172	40.371	1.00	40.18	B	C
ATOM	3246	CB	ASP	B	293	22.551	40.010	39.789	1.00	40.75	B	C
ATOM	3247	CG	ASP	B	293	22.969	41.428	39.508	1.00	39.93	B	C
ATOM	3248	OD1	ASP	B	293	23.770	41.635	38.578	1.00	43.70	B	O
ATOM	3249	OD2	ASP	B	293	22.510	42.336	40.227	1.00	42.04	B	O
ATOM	3250	C	ASP	B	293	23.084	37.986	41.124	1.00	38.77	B	C
ATOM	3251	O	ASP	B	293	22.442	38.175	42.157	1.00	36.99	B	O
ATOM	3252	N	TYR	B	294	23.288	36.770	40.628	1.00	38.33	B	N
ATOM	3253	CA	TYR	B	294	22.704	35.607	41.284	1.00	36.46	B	C

ATOM	3254	CB	TYR	B	294	21.721	34.923	40.324	1.00	37.01	B	C
ATOM	3255	CG	TYR	B	294	20.645	35.862	39.813	1.00	36.29	B	C
ATOM	3256	CD1	TYR	B	294	20.894	36.732	38.747	1.00	36.77	B	C
ATOM	3257	CE1	TYR	B	294	19.932	37.650	38.324	1.00	35.17	B	C
ATOM	3258	CD2	TYR	B	294	19.405	35.931	40.440	1.00	33.86	B	C
ATOM	3259	CE2	TYR	B	294	18.438	36.841	40.029	1.00	34.67	B	C
ATOM	3260	CZ	TYR	B	294	18.707	37.700	38.974	1.00	36.81	B	C
ATOM	3261	OH	TYR	B	294	17.747	38.614	38.586	1.00	37.64	B	O
ATOM	3262	C	TYR	B	294	23.674	34.573	41.855	1.00	35.29	B	C
ATOM	3263	O	TYR	B	294	23.241	33.612	42.482	1.00	33.83	B	O
ATOM	3264	N	LEU	B	295	24.975	34.768	41.664	1.00	34.16	B	N
ATOM	3265	CA	LEU	B	295	25.946	33.804	42.180	1.00	34.73	B	C
ATOM	3266	CB	LEU	B	295	27.191	33.790	41.287	1.00	35.44	B	C
ATOM	3267	CG	LEU	B	295	26.941	33.402	39.822	1.00	37.31	B	C
ATOM	3268	CD1	LEU	B	295	28.232	33.537	39.015	1.00	38.09	B	C
ATOM	3269	CD2	LEU	B	295	26.409	31.974	39.754	1.00	37.09	B	C
ATOM	3270	C	LEU	B	295	26.340	34.071	43.635	1.00	33.23	B	C
ATOM	3271	O	LEU	B	295	26.485	35.220	44.045	1.00	33.47	B	O
ATOM	3272	N	PRO	B	296	26.501	33.003	44.438	1.00	32.82	B	N
ATOM	3273	CD	PRO	B	296	26.174	31.603	44.099	1.00	32.14	B	C
ATOM	3274	CA	PRO	B	296	26.877	33.123	45.852	1.00	32.58	B	C
ATOM	3275	CB	PRO	B	296	26.408	31.796	46.442	1.00	30.74	B	C
ATOM	3276	CG	PRO	B	296	26.654	30.841	45.321	1.00	30.81	B	C
ATOM	3277	C	PRO	B	296	28.380	33.355	46.069	1.00	34.00	B	C
ATOM	3278	O	PRO	B	296	29.185	33.190	45.150	1.00	32.17	B	O
ATOM	3279	N	PRO	B	297	28.771	33.744	47.297	1.00	35.08	B	N
ATOM	3280	CD	PRO	B	297	27.894	34.068	48.438	1.00	34.25	B	C
ATOM	3281	CA	PRO	B	297	30.174	33.999	47.639	1.00	36.33	B	C
ATOM	3282	CB	PRO	B	297	30.111	34.293	49.137	1.00	34.76	B	C
ATOM	3283	CG	PRO	B	297	28.777	34.948	49.287	1.00	34.10	B	C
ATOM	3284	C	PRO	B	297	31.128	32.840	47.314	1.00	37.57	B	C
ATOM	3285	O	PRO	B	297	32.097	33.021	46.583	1.00	39.23	B	O
ATOM	3286	N	GLU	B	298	30.847	31.654	47.848	1.00	38.80	B	N
ATOM	3287	CA	GLU	B	298	31.709	30.491	47.626	1.00	40.63	B	C
ATOM	3288	CB	GLU	B	298	31.108	29.232	48.260	1.00	39.54	B	C
ATOM	3289	CG	GLU	B	298	29.823	28.761	47.590	1.00	38.57	B	C
ATOM	3290	CD	GLU	B	298	28.592	29.251	48.313	1.00	37.66	B	C
ATOM	3291	OE1	GLU	B	298	28.601	30.406	48.795	1.00	38.14	B	O
ATOM	3292	OE2	GLU	B	298	27.618	28.481	48.400	1.00	36.41	B	O
ATOM	3293	C	GLU	B	298	32.016	30.187	46.164	1.00	42.36	B	C
ATOM	3294	O	GLU	B	298	32.873	29.355	45.874	1.00	42.42	B	O
ATOM	3295	N	MET	B	299	31.317	30.837	45.241	1.00	44.46	B	N
ATOM	3296	CA	MET	B	299	31.572	30.589	43.830	1.00	46.93	B	C
ATOM	3297	CB	MET	B	299	30.262	30.454	43.054	1.00	47.22	B	C
ATOM	3298	CG	MET	B	299	29.494	29.190	43.410	1.00	49.38	B	C
ATOM	3299	SD	MET	B	299	28.411	28.637	42.093	1.00	51.57	B	S
ATOM	3300	CE	MET	B	299	29.502	27.513	41.247	1.00	53.08	B	C
ATOM	3301	C	MET	B	299	32.447	31.662	43.212	1.00	47.79	B	C
ATOM	3302	O	MET	B	299	33.416	31.350	42.522	1.00	48.57	B	O
ATOM	3303	N	ILE	B	300	32.118	32.926	43.457	1.00	48.73	B	N
ATOM	3304	CA	ILE	B	300	32.930	34.004	42.914	1.00	49.57	B	C
ATOM	3305	CB	ILE	B	300	32.190	35.362	42.968	1.00	49.76	B	C
ATOM	3306	CG2	ILE	B	300	30.896	35.273	42.171	1.00	49.66	B	C
ATOM	3307	CG1	ILE	B	300	31.904	35.761	44.416	1.00	48.39	B	C
ATOM	3308	CD1	ILE	B	300	31.295	37.143	44.540	1.00	47.07	B	C
ATOM	3309	C	ILE	B	300	34.243	34.096	43.697	1.00	50.74	B	C
ATOM	3310	O	ILE	B	300	35.253	34.571	43.177	1.00	50.30	B	O
ATOM	3311	N	GLU	B	301	34.226	33.630	44.943	1.00	52.24	B	N
ATOM	3312	CA	GLU	B	301	35.424	33.648	45.776	1.00	54.57	B	C
ATOM	3313	CB	GLU	B	301	35.058	33.596	47.267	1.00	55.69	B	C
ATOM	3314	CG	GLU	B	301	34.210	34.770	47.737	1.00	58.62	B	C
ATOM	3315	CD	GLU	B	301	34.020	34.806	49.247	1.00	59.50	B	C
ATOM	3316	OE1	GLU	B	301	33.827	33.731	49.855	1.00	60.80	B	O
ATOM	3317	OE2	GLU	B	301	34.046	35.915	49.823	1.00	59.81	B	O
ATOM	3318	C	GLU	B	301	36.309	32.456	45.421	1.00	55.44	B	C
ATOM	3319	O	GLU	B	301	37.419	32.322	45.936	1.00	55.50	B	O
ATOM	3320	N	GLY	B	302	35.804	31.590	44.544	1.00	55.63	B	N
ATOM	3321	CA	GLY	B	302	36.567	30.429	44.119	1.00	56.55	B	C
ATOM	3322	C	GLY	B	302	36.457	29.193	44.995	1.00	57.16	B	C
ATOM	3323	O	GLY	B	302	36.823	28.100	44.563	1.00	57.49	B	O
ATOM	3324	N	ARG	B	303	35.966	29.359	46.221	1.00	57.72	B	N
ATOM	3325	CA	ARG	B	303	35.808	28.241	47.149	1.00	57.79	B	C

ATOM	3326	CB	ARG	B	303	35.094	28.702	48.419	1.00	58.72	B	C
ATOM	3327	CG	ARG	B	303	35.855	29.706	49.257	1.00	61.00	B	C
ATOM	3328	CD	ARG	B	303	34.963	30.239	50.366	1.00	62.94	B	C
ATOM	3329	NE	ARG	B	303	35.680	31.094	51.309	1.00	64.60	B	N
ATOM	3330	CZ	ARG	B	303	36.606	30.661	52.160	1.00	65.49	B	C
ATOM	3331	NH1	ARG	B	303	37.203	31.514	52.982	1.00	65.70	B	N
ATOM	3332	NH2	ARG	B	303	36.936	29.376	52.191	1.00	65.53	B	N
ATOM	3333	C	ARG	B	303	34.995	27.119	46.517	1.00	58.00	B	C
ATOM	3334	O	ARG	B	303	34.586	27.209	45.358	1.00	58.81	B	O
ATOM	3335	N	MET	B	304	34.758	26.060	47.284	1.00	57.39	B	N
ATOM	3336	CA	MET	B	304	33.974	24.934	46.792	1.00	56.99	B	C
ATOM	3337	CB	MET	B	304	34.389	23.647	47.508	1.00	59.63	B	C
ATOM	3338	CG	MET	B	304	34.471	22.435	46.594	1.00	63.14	B	C
ATOM	3339	SD	MET	B	304	32.911	22.046	45.769	1.00	67.12	B	S
ATOM	3340	CE	MET	B	304	32.278	20.749	46.851	1.00	66.78	B	C
ATOM	3341	C	MET	B	304	32.504	25.247	47.072	1.00	54.74	B	C
ATOM	3342	O	MET	B	304	32.197	26.264	47.691	1.00	53.70	B	O
ATOM	3343	N	HIS	B	305	31.600	24.382	46.618	1.00	52.40	B	N
ATOM	3344	CA	HIS	B	305	30.170	24.598	46.826	1.00	49.37	B	C
ATOM	3345	CB	HIS	B	305	29.638	25.583	45.791	1.00	49.86	B	C
ATOM	3346	CG	HIS	B	305	29.857	25.138	44.380	1.00	51.90	B	C
ATOM	3347	CD2	HIS	B	305	28.986	24.712	43.434	1.00	52.04	B	C
ATOM	3348	ND1	HIS	B	305	31.110	25.069	43.809	1.00	51.78	B	N
ATOM	3349	CE1	HIS	B	305	31.000	24.619	42.571	1.00	53.53	B	C
ATOM	3350	NE2	HIS	B	305	29.723	24.395	42.319	1.00	53.06	B	N
ATOM	3351	C	HIS	B	305	29.347	23.312	46.750	1.00	46.97	B	C
ATOM	3352	O	HIS	B	305	29.791	22.296	46.208	1.00	46.30	B	O
ATOM	3353	N	ASP	B	306	28.135	23.372	47.289	1.00	43.16	B	N
ATOM	3354	CA	ASP	B	306	27.246	22.224	47.279	1.00	40.92	B	C
ATOM	3355	CB	ASP	B	306	27.405	21.433	48.586	1.00	40.71	B	C
ATOM	3356	CG	ASP	B	306	26.952	22.210	49.805	1.00	40.75	B	C
ATOM	3357	OD1	ASP	B	306	26.828	23.449	49.725	1.00	40.70	B	O
ATOM	3358	OD2	ASP	B	306	26.729	21.574	50.853	1.00	42.16	B	O
ATOM	3359	C	ASP	B	306	25.797	22.670	47.077	1.00	39.86	B	C
ATOM	3360	O	ASP	B	306	25.545	23.734	46.505	1.00	39.27	B	O
ATOM	3361	N	GLU	B	307	24.851	21.858	47.542	1.00	37.39	B	N
ATOM	3362	CA	GLU	B	307	23.437	22.179	47.392	1.00	35.90	B	C
ATOM	3363	CB	GLU	B	307	22.562	21.048	47.939	1.00	37.19	B	C
ATOM	3364	CG	GLU	B	307	23.310	19.796	48.370	1.00	42.69	B	C
ATOM	3365	CD	GLU	B	307	23.978	19.942	49.723	1.00	43.86	B	C
ATOM	3366	OE1	GLU	B	307	23.275	20.245	50.713	1.00	46.08	B	O
ATOM	3367	OE2	GLU	B	307	25.205	19.747	49.798	1.00	45.78	B	O
ATOM	3368	C	GLU	B	307	23.049	23.484	48.083	1.00	34.05	B	C
ATOM	3369	O	GLU	B	307	21.948	24.005	47.862	1.00	30.38	B	O
ATOM	3370	N	LYS	B	308	23.953	24.017	48.905	1.00	29.97	B	N
ATOM	3371	CA	LYS	B	308	23.660	25.247	49.632	1.00	27.77	B	C
ATOM	3372	CB	LYS	B	308	24.706	25.485	50.723	1.00	29.00	B	C
ATOM	3373	CG	LYS	B	308	24.669	24.472	51.857	1.00	30.48	B	C
ATOM	3374	CD	LYS	B	308	23.346	24.521	52.605	1.00	31.68	B	C
ATOM	3375	CE	LYS	B	308	23.442	23.788	53.921	1.00	32.64	B	C
ATOM	3376	NZ	LYS	B	308	22.194	23.897	54.726	1.00	32.70	B	N
ATOM	3377	C	LYS	B	308	23.536	26.485	48.743	1.00	25.47	B	C
ATOM	3378	O	LYS	B	308	23.007	27.504	49.177	1.00	23.55	B	O
ATOM	3379	N	VAL	B	309	24.011	26.405	47.504	1.00	23.68	B	N
ATOM	3380	CA	VAL	B	309	23.894	27.549	46.612	1.00	23.94	B	C
ATOM	3381	CB	VAL	B	309	24.666	27.334	45.284	1.00	23.56	B	C
ATOM	3382	CG1	VAL	B	309	26.147	27.135	45.572	1.00	26.07	B	C
ATOM	3383	CG2	VAL	B	309	24.101	26.148	44.528	1.00	23.94	B	C
ATOM	3384	C	VAL	B	309	22.423	27.853	46.291	1.00	24.19	B	C
ATOM	3385	O	VAL	B	309	22.051	29.017	46.139	1.00	25.34	B	O
ATOM	3386	N	ASP	B	310	21.589	26.815	46.197	1.00	23.71	B	N
ATOM	3387	CA	ASP	B	310	20.169	27.007	45.897	1.00	22.68	B	C
ATOM	3388	CB	ASP	B	310	19.454	25.656	45.690	1.00	23.58	B	C
ATOM	3389	CG	ASP	B	310	19.924	24.934	44.434	1.00	27.55	B	C
ATOM	3390	OD1	ASP	B	310	20.273	25.612	43.445	1.00	28.81	B	O
ATOM	3391	OD2	ASP	B	310	19.936	23.688	44.419	1.00	31.31	B	O
ATOM	3392	C	ASP	B	310	19.466	27.816	46.983	1.00	21.05	B	C
ATOM	3393	O	ASP	B	310	18.512	28.545	46.701	1.00	20.77	B	O
ATOM	3394	N	LEU	B	311	19.935	27.690	48.222	1.00	20.13	B	N
ATOM	3395	CA	LEU	B	311	19.353	28.444	49.327	1.00	19.16	B	C
ATOM	3396	CB	LEU	B	311	19.885	27.942	50.676	1.00	19.21	B	C
ATOM	3397	CG	LEU	B	311	19.208	26.743	51.357	1.00	21.60	B	C

ATOM	3398	CD1	LEU	B	311	17.737	27.054	51.572	1.00	20.35	B C
ATOM	3399	CD2	LEU	B	311	19.360	25.484	50.528	1.00	19.65	B C
ATOM	3400	C	LEU	B	311	19.664	29.934	49.174	1.00	19.50	B C
ATOM	3401	O	LEU	B	311	18.853	30.791	49.530	1.00	17.78	B O
ATOM	3402	N	TRP	B	312	20.848	30.245	48.653	1.00	20.26	B N
ATOM	3403	CA	TRP	B	312	21.226	31.634	48.452	1.00	19.28	B C
ATOM	3404	CB	TRP	B	312	22.716	31.729	48.109	1.00	20.45	B C
ATOM	3405	CG	TRP	B	312	23.156	33.064	47.620	1.00	18.65	B C
ATOM	3406	CD2	TRP	B	312	23.784	34.092	48.390	1.00	19.00	B C
ATOM	3407	CE2	TRP	B	312	24.034	35.176	47.515	1.00	18.21	B C
ATOM	3408	CE3	TRP	B	312	24.161	34.205	49.733	1.00	20.36	B C
ATOM	3409	CD1	TRP	B	312	23.048	33.551	46.344	1.00	20.44	B C
ATOM	3410	NE1	TRP	B	312	23.574	34.820	46.274	1.00	19.77	B N
ATOM	3411	CZ2	TRP	B	312	24.646	36.354	47.940	1.00	18.87	B C
ATOM	3412	CZ3	TRP	B	312	24.771	35.379	50.157	1.00	19.61	B C
ATOM	3413	CH2	TRP	B	312	25.007	36.438	49.260	1.00	21.25	B C
ATOM	3414	C	TRP	B	312	20.389	32.206	47.326	1.00	20.24	B C
ATOM	3415	O	TRP	B	312	19.903	33.334	47.408	1.00	18.37	B O
ATOM	3416	N	SER	B	313	20.236	31.421	46.263	1.00	20.08	B N
ATOM	3417	CA	SER	B	313	19.455	31.845	45.113	1.00	19.43	B C
ATOM	3418	CB	SER	B	313	19.460	30.760	44.037	1.00	20.79	B C
ATOM	3419	OG	SER	B	313	20.741	30.657	43.448	1.00	24.62	B O
ATOM	3420	C	SER	B	313	18.024	32.156	45.502	1.00	19.39	B C
ATOM	3421	O	SER	B	313	17.403	33.035	44.920	1.00	18.50	B O
ATOM	3422	N	LEU	B	314	17.512	31.442	46.498	1.00	19.22	B N
ATOM	3423	CA	LEU	B	314	16.141	31.641	46.960	1.00	19.58	B C
ATOM	3424	CB	LEU	B	314	15.737	30.476	47.871	1.00	20.69	B C
ATOM	3425	CG	LEU	B	314	14.276	30.024	47.987	1.00	23.50	B C
ATOM	3426	CD1	LEU	B	314	13.682	29.761	46.608	1.00	20.26	B C
ATOM	3427	CD2	LEU	B	314	14.215	28.758	48.843	1.00	20.22	B C
ATOM	3428	C	LEU	B	314	16.021	32.976	47.693	1.00	19.00	B C
ATOM	3429	O	LEU	B	314	14.973	33.637	47.632	1.00	20.65	B O
ATOM	3430	N	GLY	B	315	17.097	33.372	48.375	1.00	17.95	B N
ATOM	3431	CA	GLY	B	315	17.112	34.638	49.097	1.00	14.32	B C
ATOM	3432	C	GLY	B	315	17.085	35.805	48.120	1.00	15.06	B C
ATOM	3433	O	GLY	B	315	16.308	36.753	48.270	1.00	15.06	B O
ATOM	3434	N	VAL	B	316	17.930	35.728	47.098	1.00	15.22	B N
ATOM	3435	CA	VAL	B	316	17.996	36.775	46.090	1.00	15.50	B C
ATOM	3436	CB	VAL	B	316	19.113	36.487	45.050	1.00	17.46	B C
ATOM	3437	CG1	VAL	B	316	19.005	37.470	43.858	1.00	15.92	B C
ATOM	3438	CG2	VAL	B	316	20.492	36.626	45.715	1.00	15.82	B C
ATOM	3439	C	VAL	B	316	16.651	36.899	45.387	1.00	15.41	B C
ATOM	3440	O	VAL	B	316	16.152	38.004	45.193	1.00	18.18	B O
ATOM	3441	N	LEU	B	317	16.063	35.764	45.020	1.00	15.83	B N
ATOM	3442	CA	LEU	B	317	14.762	35.729	44.350	1.00	17.96	B C
ATOM	3443	CB	LEU	B	317	14.399	34.276	44.019	1.00	22.63	B C
ATOM	3444	CG	LEU	B	317	14.200	33.825	42.569	1.00	28.46	B C
ATOM	3445	CD1	LEU	B	317	15.254	34.441	41.657	1.00	30.81	B C
ATOM	3446	CD2	LEU	B	317	14.273	32.299	42.512	1.00	30.80	B C
ATOM	3447	C	LEU	B	317	13.653	36.359	45.204	1.00	17.12	B C
ATOM	3448	O	LEU	B	317	12.877	37.184	44.721	1.00	17.94	B O
ATOM	3449	N	CYS	B	318	13.575	35.961	46.472	1.00	15.77	B N
ATOM	3450	CA	CYS	B	318	12.569	36.494	47.386	1.00	13.11	B C
ATOM	3451	CB	CYS	B	318	12.718	35.837	48.762	1.00	12.76	B C
ATOM	3452	SG	CYS	B	318	11.422	36.262	49.915	1.00	14.06	B S
ATOM	3453	C	CYS	B	318	12.683	38.017	47.521	1.00	14.34	B C
ATOM	3454	O	CYS	B	318	11.672	38.730	47.550	1.00	17.24	B O
ATOM	3455	N	TYR	B	319	13.913	38.513	47.611	1.00	15.07	B N
ATOM	3456	CA	TYR	B	319	14.149	39.950	47.726	1.00	15.31	B C
ATOM	3457	CB	TYR	B	319	15.642	40.217	47.992	1.00	17.63	B C
ATOM	3458	CG	TYR	B	319	16.029	41.679	48.141	1.00	18.67	B C
ATOM	3459	CD1	TYR	B	319	16.103	42.524	47.032	1.00	20.95	B C
ATOM	3460	CE1	TYR	B	319	16.465	43.878	47.172	1.00	22.71	B C
ATOM	3461	CD2	TYR	B	319	16.327	42.215	49.398	1.00	21.26	B C
ATOM	3462	CE2	TYR	B	319	16.687	43.560	49.552	1.00	22.44	B C
ATOM	3463	CZ	TYR	B	319	16.752	44.384	48.436	1.00	23.40	B C
ATOM	3464	OH	TYR	B	319	17.074	45.713	48.592	1.00	22.93	B O
ATOM	3465	C	TYR	B	319	13.719	40.650	46.430	1.00	15.75	B C
ATOM	3466	O	TYR	B	319	13.009	41.655	46.461	1.00	15.99	B O
ATOM	3467	N	GLU	B	320	14.156	40.125	45.289	1.00	14.73	B N
ATOM	3468	CA	GLU	B	320	13.782	40.736	44.021	1.00	17.64	B C

ATOM	3469	CB	GLU	B	320	14.463	40.031	42.853	1.00	17.46	B	C
ATOM	3470	CG	GLU	B	320	14.174	40.726	41.542	1.00	22.76	B	C
ATOM	3471	CD	GLU	B	320	15.125	40.341	40.423	1.00	26.48	B	C
ATOM	3472	OE1	GLU	B	320	15.023	40.974	39.359	1.00	28.28	B	O
ATOM	3473	OE2	GLU	B	320	15.967	39.426	40.592	1.00	26.81	B	O
ATOM	3474	C	GLU	B	320	12.264	40.748	43.811	1.00	17.10	B	C
ATOM	3475	O	GLU	B	320	11.719	41.682	43.237	1.00	20.22	B	O
ATOM	3476	N	PHE	B	321	11.573	39.720	44.276	1.00	17.49	B	N
ATOM	3477	CA	PHE	B	321	10.126	39.703	44.121	1.00	18.22	B	C
ATOM	3478	CB	PHE	B	321	9.524	38.385	44.622	1.00	18.69	B	C
ATOM	3479	CG	PHE	B	321	9.701	37.231	43.683	1.00	21.02	B	C
ATOM	3480	CD1	PHE	B	321	10.056	37.439	42.351	1.00	21.40	B	C
ATOM	3481	CD2	PHE	B	321	9.498	35.930	44.126	1.00	22.14	B	C
ATOM	3482	CE1	PHE	B	321	10.209	36.366	41.479	1.00	21.40	B	C
ATOM	3483	CE2	PHE	B	321	9.648	34.853	43.260	1.00	23.29	B	C
ATOM	3484	CZ	PHE	B	321	10.006	35.073	41.935	1.00	22.08	B	C
ATOM	3485	C	PHE	B	321	9.469	40.841	44.887	1.00	20.00	B	C
ATOM	3486	O	PHE	B	321	8.563	41.499	44.375	1.00	19.40	B	O
ATOM	3487	N	LEU	B	322	9.919	41.057	46.123	1.00	20.34	B	N
ATOM	3488	CA	LEU	B	322	9.351	42.089	46.991	1.00	21.70	B	C
ATOM	3489	CB	LEU	B	322	9.645	41.760	48.459	1.00	20.38	B	C
ATOM	3490	CG	LEU	B	322	8.924	40.530	49.008	1.00	20.56	B	C
ATOM	3491	CD1	LEU	B	322	9.485	40.164	50.385	1.00	21.26	B	C
ATOM	3492	CD2	LEU	B	322	7.427	40.822	49.085	1.00	17.17	B	C
ATOM	3493	C	LEU	B	322	9.796	43.516	46.719	1.00	22.34	B	C
ATOM	3494	O	LEU	B	322	9.027	44.451	46.927	1.00	23.00	B	O
ATOM	3495	N	VAL	B	323	11.024	43.679	46.247	1.00	22.63	B	N
ATOM	3496	CA	VAL	B	323	11.571	45.006	45.994	1.00	24.72	B	C
ATOM	3497	CB	VAL	B	323	13.034	45.072	46.495	1.00	22.95	B	C
ATOM	3498	CG1	VAL	B	323	13.655	46.414	46.172	1.00	24.04	B	C
ATOM	3499	CG2	VAL	B	323	13.054	44.856	48.002	1.00	23.23	B	C
ATOM	3500	C	VAL	B	323	11.486	45.443	44.535	1.00	25.81	B	C
ATOM	3501	O	VAL	B	323	11.200	46.606	44.245	1.00	25.53	B	O
ATOM	3502	N	GLY	B	324	11.730	44.516	43.617	1.00	25.39	B	N
ATOM	3503	CA	GLY	B	324	11.651	44.857	42.213	1.00	25.94	B	C
ATOM	3504	C	GLY	B	324	12.980	44.762	41.508	1.00	26.51	B	C
ATOM	3505	O	GLY	B	324	13.024	44.751	40.282	1.00	27.88	B	O
ATOM	3506	N	LYS	B	325	14.062	44.709	42.281	1.00	27.18	B	N
ATOM	3507	CA	LYS	B	325	15.407	44.599	41.732	1.00	28.30	B	C
ATOM	3508	CB	LYS	B	325	16.040	45.985	41.573	1.00	32.53	B	C
ATOM	3509	CG	LYS	B	325	16.057	46.809	42.843	1.00	36.71	B	C
ATOM	3510	CD	LYS	B	325	16.678	48.183	42.605	1.00	41.59	B	C
ATOM	3511	CE	LYS	B	325	16.621	49.053	43.864	1.00	44.11	B	C
ATOM	3512	NZ	LYS	B	325	17.286	48.415	45.044	1.00	44.74	B	N
ATOM	3513	C	LYS	B	325	16.259	43.749	42.666	1.00	28.12	B	C
ATOM	3514	O	LYS	B	325	15.730	43.606	43.845	1.00	26.18	B	O
ATOM	3515	N	PRO	B	326	17.348	43.160	42.147	1.00	26.86	B	N
ATOM	3516	CD	PRO	B	326	17.790	43.134	40.742	1.00	26.79	B	C
ATOM	3517	CA	PRO	B	326	18.212	42.330	42.991	1.00	26.22	B	C
ATOM	3518	CB	PRO	B	326	19.137	41.653	41.979	1.00	27.30	B	C
ATOM	3519	CG	PRO	B	326	19.215	42.656	40.863	1.00	26.82	B	C
ATOM	3520	C	PRO	B	326	18.952	43.159	44.048	1.00	25.76	B	C
ATOM	3521	O	PRO	B	326	19.249	44.330	43.838	1.00	24.87	B	O
ATOM	3522	N	PRO	B	327	19.257	42.546	45.201	1.00	25.19	B	N
ATOM	3523	CD	PRO	B	327	19.005	41.111	45.435	1.00	24.23	B	C
ATOM	3524	CA	PRO	B	327	19.945	43.148	46.350	1.00	24.63	B	C
ATOM	3525	CB	PRO	B	327	19.864	42.046	47.407	1.00	23.95	B	C
ATOM	3526	CG	PRO	B	327	19.947	40.801	46.589	1.00	24.61	B	C
ATOM	3527	C	PRO	B	327	21.376	43.684	46.198	1.00	25.54	B	C
ATOM	3528	O	PRO	B	327	21.766	44.598	46.917	1.00	23.51	B	O
ATOM	3529	N	PHE	B	328	22.158	43.128	45.280	1.00	27.17	B	N
ATOM	3530	CA	PHE	B	328	23.540	43.572	45.107	1.00	27.57	B	C
ATOM	3531	CB	PHE	B	328	24.480	42.365	45.205	1.00	24.24	B	C
ATOM	3532	CG	PHE	B	328	24.257	41.519	46.432	1.00	23.37	B	C
ATOM	3533	CD1	PHE	B	328	24.674	41.964	47.694	1.00	21.17	B	C
ATOM	3534	CD2	PHE	B	328	23.609	40.286	46.334	1.00	20.04	B	C
ATOM	3535	CE1	PHE	B	328	24.449	41.195	48.832	1.00	19.30	B	C
ATOM	3536	CE2	PHE	B	328	23.377	39.505	47.465	1.00	21.16	B	C
ATOM	3537	CZ	PHE	B	328	23.801	39.963	48.725	1.00	21.41	B	C
ATOM	3538	C	PHE	B	328	23.778	44.306	43.786	1.00	30.91	B	C
ATOM	3539	O	PHE	B	328	24.920	44.593	43.424	1.00	29.74	B	O
ATOM	3540	N	GLU	B	329	22.699	44.617	43.073	1.00	35.49	B	N

ATOM	3541	CA	GLU	B	329	22.809	45.312	41.792	1.00	39.40	B	C
ATOM	3542	CB	GLU	B	329	21.422	45.680	41.257	1.00	40.82	B	C
ATOM	3543	CG	GLU	B	329	21.439	46.221	39.829	1.00	44.77	B	C
ATOM	3544	CD	GLU	B	329	20.104	46.816	39.401	1.00	45.81	B	C
ATOM	3545	OE1	GLU	B	329	19.695	47.839	39.986	1.00	46.10	B	O
ATOM	3546	OE2	GLU	B	329	19.465	46.262	38.480	1.00	47.31	B	O
ATOM	3547	C	GLU	B	329	23.643	46.579	41.920	1.00	41.08	B	C
ATOM	3548	O	GLU	B	329	23.353	47.444	42.740	1.00	40.70	B	O
ATOM	3549	N	ALA	B	330	24.686	46.678	41.106	1.00	43.84	B	N
ATOM	3550	CA	ALA	B	330	25.554	47.848	41.120	1.00	46.89	B	C
ATOM	3551	CB	ALA	B	330	26.943	47.469	41.610	1.00	45.55	B	C
ATOM	3552	C	ALA	B	330	25.633	48.417	39.709	1.00	49.66	B	C
ATOM	3553	O	ALA	B	330	25.028	47.884	38.776	1.00	50.00	B	O
ATOM	3554	N	ASN	B	331	26.382	49.500	39.556	1.00	52.10	B	N
ATOM	3555	CA	ASN	B	331	26.531	50.134	38.256	1.00	54.10	B	C
ATOM	3556	CB	ASN	B	331	26.785	51.634	38.436	1.00	55.63	B	C
ATOM	3557	CG	ASN	B	331	26.419	52.446	37.205	1.00	57.22	B	C
ATOM	3558	OD1	ASN	B	331	26.304	53.671	37.271	1.00	57.48	B	O
ATOM	3559	ND2	ASN	B	331	26.240	51.768	36.074	1.00	58.16	B	N
ATOM	3560	C	ASN	B	331	27.691	49.481	37.513	1.00	54.40	B	C
ATOM	3561	O	ASN	B	331	27.748	49.517	36.286	1.00	54.29	B	O
ATOM	3562	N	THR	B	332	28.602	48.867	38.266	1.00	55.19	B	N
ATOM	3563	CA	THR	B	332	29.761	48.202	37.676	1.00	55.71	B	C
ATOM	3564	CB	THR	B	332	31.056	49.020	37.908	1.00	55.73	B	C
ATOM	3565	OG1	THR	B	332	32.189	48.248	37.491	1.00	56.87	B	O
ATOM	3566	CG2	THR	B	332	31.210	49.385	39.371	1.00	56.37	B	C
ATOM	3567	C	THR	B	332	29.977	46.787	38.206	1.00	56.55	B	C
ATOM	3568	O	THR	B	332	29.604	46.466	39.337	1.00	57.13	B	O
ATOM	3569	N	TYR	B	333	30.587	45.945	37.377	1.00	56.97	B	N
ATOM	3570	CA	TYR	B	333	30.861	44.558	37.739	1.00	56.81	B	C
ATOM	3571	CB	TYR	B	333	31.623	43.848	36.610	1.00	58.85	B	C
ATOM	3572	CG	TYR	B	333	30.984	43.930	35.233	1.00	62.30	B	C
ATOM	3573	CD1	TYR	B	333	31.675	43.490	34.099	1.00	62.80	B	C
ATOM	3574	CE1	TYR	B	333	31.103	43.563	32.826	1.00	63.19	B	C
ATOM	3575	CD2	TYR	B	333	29.695	44.446	35.057	1.00	63.26	B	C
ATOM	3576	CE2	TYR	B	333	29.114	44.521	33.786	1.00	63.66	B	C
ATOM	3577	CZ	TYR	B	333	29.825	44.079	32.678	1.00	63.50	B	C
ATOM	3578	OH	TYR	B	333	29.257	44.153	31.425	1.00	63.78	B	O
ATOM	3579	C	TYR	B	333	31.697	44.484	39.012	1.00	55.92	B	C
ATOM	3580	O	TYR	B	333	31.351	43.770	39.950	1.00	56.04	B	O
ATOM	3581	N	GLN	B	334	32.802	45.224	39.033	1.00	55.18	B	N
ATOM	3582	CA	GLN	B	334	33.711	45.227	40.176	1.00	54.38	B	C
ATOM	3583	CB	GLN	B	334	34.871	46.203	39.925	1.00	55.19	B	C
ATOM	3584	CG	GLN	B	334	34.482	47.678	39.879	1.00	57.42	B	C
ATOM	3585	CD	GLN	B	334	35.599	48.566	39.340	1.00	59.56	B	C
ATOM	3586	OE1	GLN	B	334	36.756	48.459	39.759	1.00	60.33	B	O
ATOM	3587	NE2	GLN	B	334	35.253	49.454	38.409	1.00	59.33	B	N
ATOM	3588	C	GLN	B	334	32.998	45.572	41.478	1.00	53.11	B	C
ATOM	3589	O	GLN	B	334	33.352	45.067	42.544	1.00	52.68	B	O
ATOM	3590	N	GLU	B	335	31.986	46.427	41.386	1.00	51.38	B	N
ATOM	3591	CA	GLU	B	335	31.226	46.826	42.561	1.00	50.81	B	C
ATOM	3592	CB	GLU	B	335	30.428	48.098	42.257	1.00	51.54	B	C
ATOM	3593	CG	GLU	B	335	29.750	48.707	43.470	1.00	54.47	B	C
ATOM	3594	CD	GLU	B	335	30.722	48.982	44.607	1.00	56.00	B	C
ATOM	3595	OE1	GLU	B	335	30.265	49.435	45.681	1.00	55.50	B	O
ATOM	3596	OE2	GLU	B	335	31.939	48.745	44.429	1.00	56.77	B	O
ATOM	3597	C	GLU	B	335	30.287	45.693	42.997	1.00	49.24	B	C
ATOM	3598	O	GLU	B	335	30.247	45.321	44.171	1.00	48.26	B	O
ATOM	3599	N	THR	B	336	29.543	45.144	42.042	1.00	47.63	B	N
ATOM	3600	CA	THR	B	336	28.622	44.046	42.318	1.00	46.12	B	C
ATOM	3601	CB	THR	B	336	28.002	43.497	41.013	1.00	45.85	B	C
ATOM	3602	OG1	THR	B	336	27.289	44.548	40.347	1.00	47.48	B	O
ATOM	3603	CG2	THR	B	336	27.046	42.345	41.308	1.00	44.35	B	C
ATOM	3604	C	THR	B	336	29.394	42.922	43.001	1.00	45.04	B	C
ATOM	3605	O	THR	B	336	28.916	42.313	43.963	1.00	44.35	B	O
ATOM	3606	N	TYR	B	337	30.594	42.665	42.494	1.00	42.84	B	N
ATOM	3607	CA	TYR	B	337	31.465	41.625	43.025	1.00	42.44	B	C
ATOM	3608	CB	TYR	B	337	32.784	41.606	42.251	1.00	45.11	B	C
ATOM	3609	CG	TYR	B	337	33.675	40.446	42.624	1.00	47.49	B	C
ATOM	3610	CD1	TYR	B	337	33.639	39.258	41.901	1.00	48.63	B	C
ATOM	3611	CE1	TYR	B	337	34.421	38.166	42.273	1.00	51.33	B	C
ATOM	3612	CD2	TYR	B	337	34.520	40.520	43.733	1.00	49.23	B	C

ATOM	3613	CE2	TYR	B	337	35.302	39.439	44.114	1.00	50.54	B	C
ATOM	3614	CZ	TYR	B	337	35.247	38.263	43.380	1.00	51.96	B	C
ATOM	3615	OH	TYR	B	337	36.005	37.179	43.761	1.00	54.44	B	O
ATOM	3616	C	TYR	B	337	31.769	41.809	44.513	1.00	41.13	B	C
ATOM	3617	O	TYR	B	337	31.759	40.843	45.276	1.00	40.24	B	O
ATOM	3618	N	LYS	B	338	32.048	43.050	44.909	1.00	40.20	B	N
ATOM	3619	CA	LYS	B	338	32.371	43.390	46.296	1.00	38.23	B	C
ATOM	3620	CB	LYS	B	338	32.833	44.850	46.388	1.00	41.59	B	C
ATOM	3621	CG	LYS	B	338	34.123	45.176	45.644	1.00	44.66	B	C
ATOM	3622	CD	LYS	B	338	34.527	46.631	45.891	1.00	48.09	B	C
ATOM	3623	CE	LYS	B	338	35.874	46.981	45.256	1.00	48.00	B	C
ATOM	3624	NZ	LYS	B	338	35.838	46.925	43.765	1.00	51.10	B	N
ATOM	3625	C	LYS	B	338	31.205	43.191	47.262	1.00	35.20	B	C
ATOM	3626	O	LYS	B	338	31.339	42.526	48.291	1.00	32.57	B	O
ATOM	3627	N	ARG	B	339	30.063	43.783	46.923	1.00	33.78	B	N
ATOM	3628	CA	ARG	B	339	28.868	43.694	47.758	1.00	32.18	B	C
ATOM	3629	CB	ARG	B	339	27.741	44.499	47.125	1.00	34.50	B	C
ATOM	3630	CG	ARG	B	339	28.069	45.975	46.971	1.00	34.49	B	C
ATOM	3631	CD	ARG	B	339	26.849	46.753	46.513	1.00	37.43	B	C
ATOM	3632	NE	ARG	B	339	27.183	48.140	46.215	1.00	39.07	B	N
ATOM	3633	CZ	ARG	B	339	26.318	49.042	45.768	1.00	40.69	B	C
ATOM	3634	NH1	ARG	B	339	25.052	48.714	45.563	1.00	41.15	B	N
ATOM	3635	NH2	ARG	B	339	26.723	50.278	45.524	1.00	42.78	B	N
ATOM	3636	C	ARG	B	339	28.424	42.255	48.005	1.00	30.59	B	C
ATOM	3637	O	ARG	B	339	27.998	41.916	49.106	1.00	30.06	B	O
ATOM	3638	N	ILE	B	340	28.531	41.411	46.983	1.00	28.84	B	N
ATOM	3639	CA	ILE	B	340	28.172	40.005	47.113	1.00	28.23	B	C
ATOM	3640	CB	ILE	B	340	28.265	39.284	45.746	1.00	29.04	B	C
ATOM	3641	CG2	ILE	B	340	28.191	37.777	45.932	1.00	27.61	B	C
ATOM	3642	CG1	ILE	B	340	27.143	39.778	44.828	1.00	29.93	B	C
ATOM	3643	CD1	ILE	B	340	27.294	39.344	43.379	1.00	30.36	B	C
ATOM	3644	C	ILE	B	340	29.149	39.362	48.094	1.00	28.00	B	C
ATOM	3645	O	ILE	B	340	28.746	38.760	49.092	1.00	28.08	B	O
ATOM	3646	N	SER	B	341	30.437	39.511	47.806	1.00	27.83	B	N
ATOM	3647	CA	SER	B	341	31.500	38.971	48.647	1.00	27.74	B	C
ATOM	3648	CB	SER	B	341	32.869	39.405	48.099	1.00	29.39	B	C
ATOM	3649	OG	SER	B	341	33.904	39.101	49.023	1.00	31.17	B	O
ATOM	3650	C	SER	B	341	31.390	39.394	50.115	1.00	26.62	B	C
ATOM	3651	O	SER	B	341	31.581	38.576	51.019	1.00	26.60	B	O
ATOM	3652	N	ARG	B	342	31.095	40.670	50.349	1.00	26.86	B	N
ATOM	3653	CA	ARG	B	342	30.967	41.190	51.713	1.00	27.32	B	C
ATOM	3654	CB	ARG	B	342	31.486	42.635	51.786	1.00	30.87	B	C
ATOM	3655	CG	ARG	B	342	32.988	42.792	51.559	1.00	34.75	B	C
ATOM	3656	CD	ARG	B	342	33.407	44.264	51.585	1.00	38.59	B	C
ATOM	3657	NE	ARG	B	342	34.861	44.410	51.496	1.00	44.23	B	N
ATOM	3658	CZ	ARG	B	342	35.518	45.568	51.542	1.00	45.71	B	C
ATOM	3659	NH1	ARG	B	342	36.842	45.574	51.450	1.00	47.72	B	N
ATOM	3660	NH2	ARG	B	342	34.862	46.717	51.678	1.00	45.74	B	N
ATOM	3661	C	ARG	B	342	29.525	41.157	52.232	1.00	26.65	B	C
ATOM	3662	O	ARG	B	342	29.249	41.651	53.324	1.00	24.28	B	O
ATOM	3663	N	VAL	B	343	28.615	40.578	51.449	1.00	25.25	B	N
ATOM	3664	CA	VAL	B	343	27.201	40.491	51.825	1.00	23.45	B	C
ATOM	3665	CB	VAL	B	343	26.964	39.453	52.942	1.00	22.70	B	C
ATOM	3666	CG1	VAL	B	343	25.475	39.151	53.038	1.00	26.95	B	C
ATOM	3667	CG2	VAL	B	343	27.744	38.182	52.667	1.00	24.45	B	C
ATOM	3668	C	VAL	B	343	26.667	41.834	52.319	1.00	22.20	B	C
ATOM	3669	O	VAL	B	343	26.236	41.958	53.463	1.00	22.42	B	O
ATOM	3670	N	GLU	B	344	26.702	42.841	51.461	1.00	20.93	B	N
ATOM	3671	CA	GLU	B	344	26.224	44.163	51.836	1.00	19.95	B	C
ATOM	3672	CB	GLU	B	344	27.317	45.217	51.593	1.00	21.95	B	C
ATOM	3673	CG	GLU	B	344	28.483	45.077	52.579	1.00	26.85	B	C
ATOM	3674	CD	GLU	B	344	29.731	45.844	52.177	1.00	29.55	B	C
ATOM	3675	OE1	GLU	B	344	30.643	45.948	53.029	1.00	31.16	B	O
ATOM	3676	OE2	GLU	B	344	29.811	46.331	51.021	1.00	29.15	B	O
ATOM	3677	C	GLU	B	344	24.970	44.500	51.054	1.00	19.08	B	C
ATOM	3678	O	GLU	B	344	25.007	44.692	49.832	1.00	15.34	B	O
ATOM	3679	N	PHE	B	345	23.859	44.555	51.778	1.00	16.62	B	N
ATOM	3680	CA	PHE	B	345	22.572	44.858	51.188	1.00	19.25	B	C
ATOM	3681	CB	PHE	B	345	21.938	43.576	50.615	1.00	17.18	B	C
ATOM	3682	CG	PHE	B	345	21.524	42.574	51.661	1.00	17.47	B	C
ATOM	3683	CD1	PHE	B	345	20.271	42.645	52.253	1.00	18.52	B	C
ATOM	3684	CD2	PHE	B	345	22.394	41.561	52.060	1.00	19.11	B	C

ATOM	3685	CR1	PHE	B	345	19.884	41.725	53.225	1.00	18.14	B	C
ATOM	3686	CE2	PHE	B	345	22.015	40.634	53.039	1.00	20.48	B	C
ATOM	3687	CZ	PHE	B	345	20.758	40.719	53.620	1.00	19.36	B	C
ATOM	3688	C	PHE	B	345	21.673	45.470	52.253	1.00	18.97	B	C
ATOM	3689	O	PHE	B	345	21.857	45.229	53.450	1.00	19.32	B	O
ATOM	3690	N	THR	B	346	20.714	46.275	51.811	1.00	19.42	B	N
ATOM	3691	CA	THR	B	346	19.775	46.917	52.715	1.00	19.27	B	C
ATOM	3692	CB	THR	B	346	20.082	48.424	52.857	1.00	19.00	B	C
ATOM	3693	OG1	THR	B	346	20.109	49.030	51.564	1.00	20.30	B	O
ATOM	3694	CG2	THR	B	346	21.437	48.635	53.539	1.00	18.82	B	C
ATOM	3695	C	THR	B	346	18.350	46.704	52.197	1.00	19.39	B	C
ATOM	3696	O	THR	B	346	18.163	46.200	51.095	1.00	20.35	B	O
ATOM	3697	N	PHE	B	347	17.364	47.086	53.003	1.00	20.32	B	N
ATOM	3698	CA	PHE	B	347	15.941	46.925	52.689	1.00	22.26	B	C
ATOM	3699	CB	PHE	B	347	15.239	46.134	53.801	1.00	19.26	B	C
ATOM	3700	CG	PHE	B	347	15.710	44.715	53.954	1.00	22.00	B	C
ATOM	3701	CD1	PHE	B	347	15.318	43.731	53.050	1.00	20.34	B	C
ATOM	3702	CD2	PHE	B	347	16.521	44.352	55.029	1.00	19.14	B	C
ATOM	3703	CE1	PHE	B	347	15.723	42.411	53.217	1.00	18.46	B	C
ATOM	3704	CE2	PHE	B	347	16.930	43.037	55.202	1.00	16.81	B	C
ATOM	3705	CZ	PHE	B	347	16.529	42.062	54.293	1.00	16.52	B	C
ATOM	3706	C	PHE	B	347	15.180	48.246	52.572	1.00	23.77	B	C
ATOM	3707	O	PHE	B	347	15.384	49.166	53.364	1.00	24.75	B	O
ATOM	3708	N	PRO	B	348	14.280	48.353	51.590	1.00	26.17	B	N
ATOM	3709	CD	PRO	B	348	14.032	47.471	50.438	1.00	27.03	B	C
ATOM	3710	CA	PRO	B	348	13.519	49.602	51.474	1.00	27.72	B	C
ATOM	3711	CB	PRO	B	348	12.702	49.393	50.198	1.00	28.07	B	C
ATOM	3712	CG	PRO	B	348	13.561	48.455	49.394	1.00	28.17	B	C
ATOM	3713	C	PRO	B	348	12.629	49.609	52.727	1.00	29.25	B	C
ATOM	3714	O	PRO	B	348	12.262	48.546	53.232	1.00	29.40	B	O
ATOM	3715	N	ASP	B	349	12.265	50.784	53.220	1.00	30.11	B	N
ATOM	3716	CA	ASP	B	349	11.453	50.864	54.426	1.00	30.67	B	C
ATOM	3717	CB	ASP	B	349	11.199	52.329	54.785	1.00	35.47	B	C
ATOM	3718	CG	ASP	B	349	12.486	53.141	54.863	1.00	39.29	B	C
ATOM	3719	OD1	ASP	B	349	13.519	52.592	55.315	1.00	40.71	B	O
ATOM	3720	OD2	ASP	B	349	12.463	54.334	54.483	1.00	42.81	B	O
ATOM	3721	C	ASP	B	349	10.127	50.105	54.428	1.00	30.99	B	C
ATOM	3722	O	ASP	B	349	9.639	49.729	55.501	1.00	31.13	B	O
ATOM	3723	N	PHE	B	350	9.539	49.858	53.256	1.00	28.24	B	N
ATOM	3724	CA	PHE	B	350	8.256	49.153	53.225	1.00	24.82	B	C
ATOM	3725	CB	PHE	B	350	7.496	49.459	51.920	1.00	21.72	B	C
ATOM	3726	CG	PHE	B	350	8.175	48.964	50.670	1.00	20.48	B	C
ATOM	3727	CD1	PHE	B	350	8.133	47.616	50.323	1.00	20.47	B	C
ATOM	3728	CD2	PHE	B	350	8.836	49.853	49.825	1.00	18.76	B	C
ATOM	3729	CE1	PHE	B	350	8.741	47.156	49.145	1.00	19.61	B	C
ATOM	3730	CE2	PHE	B	350	9.447	49.412	48.649	1.00	20.75	B	C
ATOM	3731	CZ	PHE	B	350	9.400	48.057	48.305	1.00	22.07	B	C
ATOM	3732	C	PHE	B	350	8.327	47.637	53.442	1.00	25.64	B	C
ATOM	3733	O	PHE	B	350	7.293	47.002	53.660	1.00	25.56	B	O
ATOM	3734	N	VAL	B	351	9.523	47.050	53.386	1.00	23.17	B	N
ATOM	3735	CA	VAL	B	351	9.628	45.604	53.586	1.00	21.29	B	C
ATOM	3736	CB	VAL	B	351	11.012	45.072	53.124	1.00	18.96	B	C
ATOM	3737	CG1	VAL	B	351	11.060	43.564	53.314	1.00	18.55	B	C
ATOM	3738	CG2	VAL	B	351	11.244	45.423	51.663	1.00	15.50	B	C
ATOM	3739	C	VAL	B	351	9.429	45.215	55.052	1.00	21.74	B	C
ATOM	3740	O	VAL	B	351	10.054	45.772	55.949	1.00	20.28	B	O
ATOM	3741	N	THR	B	352	8.535	44.254	55.273	1.00	22.77	B	N
ATOM	3742	CA	THR	B	352	8.186	43.776	56.609	1.00	23.82	B	C
ATOM	3743	CB	THR	B	352	6.918	42.899	56.523	1.00	25.23	B	C
ATOM	3744	OG1	THR	B	352	5.829	43.705	56.054	1.00	27.41	B	O
ATOM	3745	CG2	THR	B	352	6.555	42.331	57.872	1.00	27.51	B	C
ATOM	3746	C	THR	B	352	9.304	43.017	57.343	1.00	22.96	B	C
ATOM	3747	O	THR	B	352	10.213	42.463	56.718	1.00	23.44	B	O
ATOM	3748	N	ALA	B	353	9.228	42.998	58.674	1.00	22.56	B	N
ATOM	3749	CA	ALA	B	353	10.233	42.334	59.502	1.00	19.72	B	C
ATOM	3750	CB	ALA	B	353	10.018	42.682	60.984	1.00	21.49	B	C
ATOM	3751	C	ALA	B	353	10.230	40.825	59.305	1.00	18.37	B	C
ATOM	3752	O	ALA	B	353	11.270	40.184	59.390	1.00	17.81	B	O
ATOM	3753	N	GLY	B	354	9.061	40.252	59.043	1.00	17.83	B	N
ATOM	3754	CA	GLY	B	354	9.002	38.820	58.807	1.00	14.69	B	C
ATOM	3755	C	GLY	B	354	9.749	38.486	57.524	1.00	15.67	B	C
ATOM	3756	O	GLY	B	354	10.484	37.497	57.449	1.00	15.82	B	O

ATOM	3757	N	ALA	B	355	9.571	39.318	56.503	1.00	14.39	B	N
ATOM	3758	CA	ALA	B	355	10.241	39.091	55.227	1.00	16.28	B	C
ATOM	3759	CB	ALA	B	355	9.683	40.047	54.163	1.00	14.46	B	C
ATOM	3760	C	ALA	B	355	11.759	39.285	55.374	1.00	16.62	B	C
ATOM	3761	O	ALA	B	355	12.541	38.560	54.778	1.00	18.69	B	O
ATOM	3762	N	ARG	B	356	12.162	40.266	56.175	1.00	18.54	B	N
ATOM	3763	CA	ARG	B	356	13.571	40.558	56.397	1.00	18.70	B	C
ATOM	3764	CB	ARG	B	356	13.703	41.894	57.138	1.00	19.52	B	C
ATOM	3765	CG	ARG	B	356	13.122	43.053	56.343	1.00	21.00	B	C
ATOM	3766	CD	ARG	B	356	12.584	44.189	57.208	1.00	21.75	B	C
ATOM	3767	NE	ARG	B	356	13.576	45.223	57.463	1.00	25.09	B	N
ATOM	3768	CZ	ARG	B	356	13.435	46.503	57.130	1.00	20.74	B	C
ATOM	3769	NH1	ARG	B	356	12.340	46.921	56.528	1.00	23.41	B	N
ATOM	3770	NH2	ARG	B	356	14.400	47.363	57.394	1.00	19.75	B	N
ATOM	3771	C	ARG	B	356	14.266	39.436	57.168	1.00	20.44	B	C
ATOM	3772	O	ARG	B	356	15.449	39.156	56.951	1.00	21.10	B	O
ATOM	3773	N	ASP	B	357	13.546	38.786	58.076	1.00	20.86	B	N
ATOM	3774	CA	ASP	B	357	14.164	37.698	58.819	1.00	18.80	B	C
ATOM	3775	CB	ASP	B	357	13.259	37.204	59.938	1.00	20.18	B	C
ATOM	3776	CG	ASP	B	357	13.911	36.098	60.740	1.00	19.17	B	C
ATOM	3777	OD1	ASP	B	357	14.805	36.415	61.543	1.00	20.57	B	O
ATOM	3778	OD2	ASP	B	357	13.552	34.918	60.555	1.00	21.02	B	O
ATOM	3779	C	ASP	B	357	14.465	36.530	57.887	1.00	18.01	B	C
ATOM	3780	O	ASP	B	357	15.539	35.937	57.941	1.00	19.94	B	O
ATOM	3781	N	LEU	B	358	13.508	36.199	57.029	1.00	18.45	B	N
ATOM	3782	CA	LEU	B	358	13.696	35.101	56.087	1.00	17.99	B	C
ATOM	3783	CB	LEU	B	358	12.442	34.900	55.231	1.00	17.24	B	C
ATOM	3784	CG	LEU	B	358	12.619	33.829	54.153	1.00	18.71	B	C
ATOM	3785	CD1	LEU	B	358	12.858	32.466	54.819	1.00	17.61	B	C
ATOM	3786	CD2	LEU	B	358	11.396	33.791	53.254	1.00	20.87	B	C
ATOM	3787	C	LEU	B	358	14.879	35.357	55.161	1.00	17.62	B	C
ATOM	3788	O	LEU	B	358	15.745	34.499	54.986	1.00	17.62	B	O
ATOM	3789	N	ILE	B	359	14.906	36.543	54.565	1.00	16.22	B	N
ATOM	3790	CA	ILE	B	359	15.976	36.891	53.640	1.00	19.15	B	C
ATOM	3791	CB	ILE	B	359	15.684	38.236	52.940	1.00	18.39	B	C
ATOM	3792	CG2	ILE	B	359	16.848	38.610	52.036	1.00	17.22	B	C
ATOM	3793	CG1	ILE	B	359	14.387	38.117	52.129	1.00	20.22	B	C
ATOM	3794	CD1	ILE	B	359	13.872	39.439	51.528	1.00	22.11	B	C
ATOM	3795	C	ILE	B	359	17.316	36.947	54.282	1.00	17.31	B	C
ATOM	3796	O	ILE	B	359	18.359	36.611	53.640	1.00	16.11	B	O
ATOM	3797	N	SER	B	360	17.433	37.364	55.543	1.00	16.97	B	N
ATOM	3798	CA	SER	B	360	18.725	37.447	56.213	1.00	18.07	B	C
ATOM	3799	CB	SER	B	360	18.615	38.316	57.466	1.00	18.16	B	C
ATOM	3800	OG	SER	B	360	18.402	39.669	57.111	1.00	17.16	B	O
ATOM	3801	C	SER	B	360	19.267	36.060	56.573	1.00	19.03	B	C
ATOM	3802	O	SER	B	360	20.480	35.874	56.711	1.00	18.93	B	O
ATOM	3803	N	ARG	B	361	18.369	35.088	56.716	1.00	19.00	B	N
ATOM	3804	CA	ARG	B	361	18.775	33.730	57.040	1.00	20.67	B	C
ATOM	3805	CB	ARG	B	361	17.630	33.003	57.742	1.00	25.65	B	C
ATOM	3806	CG	ARG	B	361	17.160	33.726	58.993	1.00	31.87	B	C
ATOM	3807	CD	ARG	B	361	16.083	32.947	59.716	1.00	38.15	B	C
ATOM	3808	NE	ARG	B	361	16.529	31.589	59.998	1.00	44.86	B	N
ATOM	3809	CZ	ARG	B	361	15.896	30.743	60.804	1.00	48.17	B	C
ATOM	3810	NH1	ARG	B	361	14.779	31.116	61.419	1.00	47.35	B	N
ATOM	3811	NH2	ARG	B	361	16.382	29.521	60.993	1.00	48.87	B	N
ATOM	3812	C	ARG	B	361	19.211	32.974	55.785	1.00	21.43	B	C
ATOM	3813	O	ARG	B	361	19.994	32.024	55.855	1.00	22.60	B	O
ATOM	3814	N	LEU	B	362	18.721	33.407	54.628	1.00	20.42	B	N
ATOM	3815	CA	LEU	B	362	19.087	32.763	53.375	1.00	18.53	B	C
ATOM	3816	CB	LEU	B	362	17.949	32.888	52.362	1.00	17.29	B	C
ATOM	3817	CG	LEU	B	362	16.665	32.103	52.653	1.00	15.10	B	C
ATOM	3818	CD1	LEU	B	362	15.621	32.437	51.611	1.00	15.28	B	C
ATOM	3819	CD2	LEU	B	362	16.961	30.596	52.650	1.00	14.06	B	C
ATOM	3820	C	LEU	B	362	20.364	33.370	52.794	1.00	20.19	B	C
ATOM	3821	O	LEU	B	362	21.117	32.695	52.090	1.00	19.39	B	O
ATOM	3822	N	LEU	B	363	20.614	34.640	53.098	1.00	19.15	B	N
ATOM	3823	CA	LEU	B	363	21.793	35.310	52.565	1.00	21.61	B	C
ATOM	3824	CB	LEU	B	363	21.421	36.728	52.121	1.00	21.25	B	C
ATOM	3825	CG	LEU	B	363	20.391	36.784	50.986	1.00	22.02	B	C
ATOM	3826	CD1	LEU	B	363	20.063	38.228	50.677	1.00	21.41	B	C
ATOM	3827	CD2	LEU	B	363	20.941	36.079	49.732	1.00	21.42	B	C
ATOM	3828	C	LEU	B	363	22.970	35.345	53.545	1.00	23.78	B	C

ATOM	3829	O	LEU	B	363	23.443	36.421	53.931	1.00	25.25	B	O
ATOM	3830	N	LYS	B	364	23.425	34.158	53.939	1.00	22.72	B	N
ATOM	3831	CA	LYS	B	364	24.546	34.004	54.860	1.00	25.21	B	C
ATOM	3832	CB	LYS	B	364	24.296	32.822	55.812	1.00	26.10	B	C
ATOM	3833	CG	LYS	B	364	23.328	33.116	56.964	1.00	28.20	B	C
ATOM	3834	CD	LYS	B	364	23.970	34.044	57.987	1.00	30.83	B	C
ATOM	3835	CE	LYS	B	364	22.964	34.630	58.974	1.00	33.43	B	C
ATOM	3836	NZ	LYS	B	364	22.367	33.622	59.900	1.00	36.33	B	N
ATOM	3837	C	LYS	B	364	25.831	33.766	54.062	1.00	25.33	B	C
ATOM	3838	O	LYS	B	364	25.850	32.987	53.102	1.00	24.66	B	O
ATOM	3839	N	HIS	B	365	26.904	34.444	54.455	1.00	25.93	B	N
ATOM	3840	CA	HIS	B	365	28.175	34.296	53.763	1.00	26.63	B	C
ATOM	3841	CB	HIS	B	365	29.261	35.141	54.424	1.00	25.92	B	C
ATOM	3842	CG	HIS	B	365	30.590	35.009	53.756	1.00	26.63	B	C
ATOM	3843	CD2	HIS	B	365	31.646	34.202	54.022	1.00	25.39	B	C
ATOM	3844	ND1	HIS	B	365	30.909	35.688	52.598	1.00	28.19	B	N
ATOM	3845	CE1	HIS	B	365	32.103	35.303	52.179	1.00	27.11	B	C
ATOM	3846	NE2	HIS	B	365	32.569	34.401	53.024	1.00	26.10	B	N
ATOM	3847	C	HIS	B	365	28.636	32.845	53.757	1.00	26.18	B	C
ATOM	3848	O	HIS	B	365	29.112	32.338	52.747	1.00	27.21	B	O
ATOM	3849	N	ASN	B	366	28.504	32.195	54.907	1.00	27.62	B	N
ATOM	3850	CA	ASN	B	366	28.902	30.804	55.076	1.00	29.77	B	C
ATOM	3851	CB	ASN	B	366	29.442	30.620	56.493	1.00	31.38	B	C
ATOM	3852	CG	ASN	B	366	29.794	29.190	56.802	1.00	35.31	B	C
ATOM	3853	OD1	ASN	B	366	30.346	28.480	55.963	1.00	38.20	B	O
ATOM	3854	ND2	ASN	B	366	29.491	28.757	58.020	1.00	37.60	B	N
ATOM	3855	C	ASN	B	366	27.716	29.862	54.805	1.00	28.07	B	C
ATOM	3856	O	ASN	B	366	26.771	29.793	55.583	1.00	26.33	B	O
ATOM	3857	N	PRO	B	367	27.765	29.121	53.690	1.00	29.03	B	N
ATOM	3858	CD	PRO	B	367	28.937	29.001	52.804	1.00	29.75	B	C
ATOM	3859	CA	PRO	B	367	26.711	28.182	53.285	1.00	29.22	B	C
ATOM	3860	CB	PRO	B	367	27.283	27.542	52.017	1.00	27.84	B	C
ATOM	3861	CG	PRO	B	367	28.755	27.619	52.224	1.00	29.93	B	C
ATOM	3862	C	PRO	B	367	26.285	27.148	54.323	1.00	29.89	B	C
ATOM	3863	O	PRO	B	367	25.132	26.715	54.332	1.00	30.60	B	O
ATOM	3864	N	SER	B	368	27.202	26.754	55.198	1.00	30.30	B	N
ATOM	3865	CA	SER	B	368	26.871	25.762	56.208	1.00	31.18	B	C
ATOM	3866	CB	SER	B	368	28.141	25.252	56.905	1.00	32.85	B	C
ATOM	3867	OG	SER	B	368	28.550	26.132	57.939	1.00	35.93	B	O
ATOM	3868	C	SER	B	368	25.907	26.345	57.233	1.00	30.31	B	C
ATOM	3869	O	SER	B	368	25.268	25.613	57.975	1.00	30.36	B	O
ATOM	3870	N	GLN	B	369	25.797	27.667	57.264	1.00	31.55	B	N
ATOM	3871	CA	GLN	B	369	24.897	28.333	58.200	1.00	32.07	B	C
ATOM	3872	CB	GLN	B	369	25.505	29.665	58.656	1.00	36.11	B	C
ATOM	3873	CG	GLN	B	369	26.848	29.518	59.359	1.00	42.42	B	C
ATOM	3874	CD	GLN	B	369	27.376	30.837	59.891	1.00	45.10	B	C
ATOM	3875	OE1	GLN	B	369	26.768	31.454	60.766	1.00	48.57	B	O
ATOM	3876	NE2	GLN	B	369	28.511	31.279	59.361	1.00	46.32	B	N
ATOM	3877	C	GLN	B	369	23.506	28.581	57.618	1.00	29.24	B	C
ATOM	3878	O	GLN	B	369	22.607	29.029	58.323	1.00	28.91	B	O
ATOM	3879	N	ARG	B	370	23.330	28.301	56.331	1.00	27.41	B	N
ATOM	3880	CA	ARG	B	370	22.036	28.496	55.675	1.00	25.29	B	C
ATOM	3881	CB	ARG	B	370	22.230	28.548	54.157	1.00	23.14	B	C
ATOM	3882	CG	ARG	B	370	23.078	29.715	53.698	1.00	17.66	B	C
ATOM	3883	CD	ARG	B	370	23.530	29.546	52.268	1.00	21.09	B	C
ATOM	3884	NE	ARG	B	370	24.615	30.468	51.956	1.00	20.83	B	N
ATOM	3885	CZ	ARG	B	370	25.404	30.365	50.895	1.00	22.00	B	C
ATOM	3886	NH1	ARG	B	370	25.235	29.372	50.029	1.00	21.78	B	N
ATOM	3887	NH2	ARG	B	370	26.365	31.262	50.698	1.00	23.58	B	N
ATOM	3888	C	ARG	B	370	21.096	27.348	56.048	1.00	24.43	B	C
ATOM	3889	O	ARG	B	370	21.533	26.214	56.209	1.00	25.53	B	O
ATOM	3890	N	PRO	B	371	19.789	27.625	56.177	1.00	25.63	B	N
ATOM	3891	CD	PRO	B	371	19.116	28.920	55.965	1.00	25.62	B	C
ATOM	3892	CA	PRO	B	371	18.816	26.584	56.538	1.00	25.56	B	C
ATOM	3893	CB	PRO	B	371	17.561	27.392	56.860	1.00	25.65	B	C
ATOM	3894	CG	PRO	B	371	17.649	28.519	55.882	1.00	24.95	B	C
ATOM	3895	C	PRO	B	371	18.551	25.529	55.461	1.00	25.92	B	C
ATOM	3896	O	PRO	B	371	18.942	25.689	54.308	1.00	27.40	B	O
ATOM	3897	N	MET	B	372	17.893	24.444	55.853	1.00	27.14	B	N
ATOM	3898	CA	MET	B	372	17.533	23.391	54.911	1.00	27.45	B	C
ATOM	3899	CB	MET	B	372	17.344	22.053	55.623	1.00	29.21	B	C
ATOM	3900	CG	MET	B	372	18.607	21.462	56.225	1.00	32.29	B	C

ATOM	3901	SD	MET	B	372	18.257	19.888	57.038	1.00	38.80	B S
ATOM	3902	CE	MET	B	372	18.599	18.751	55.690	1.00	36.16	B C
ATOM	3903	C	MET	B	372	16.206	23.820	54.305	1.00	26.36	B C
ATOM	3904	O	MET	B	372	15.471	24.590	54.922	1.00	27.49	B O
ATOM	3905	N	LEU	B	373	15.901	23.323	53.108	1.00	24.23	B N
ATOM	3906	CA	LEU	B	373	14.657	23.663	52.423	1.00	22.39	B C
ATOM	3907	CB	LEU	B	373	14.528	22.850	51.132	1.00	22.84	B C
ATOM	3908	CG	LEU	B	373	15.511	23.250	50.032	1.00	24.40	B C
ATOM	3909	CD1	LEU	B	373	15.332	22.333	48.825	1.00	26.89	B C
ATOM	3910	CD2	LEU	B	373	15.282	24.716	49.638	1.00	24.98	B C
ATOM	3911	C	LEU	B	373	13.412	23.470	53.272	1.00	20.58	B C
ATOM	3912	O	LEU	B	373	12.488	24.280	53.212	1.00	22.00	B O
ATOM	3913	N	ALA	B	374	13.393	22.409	54.071	1.00	21.21	B N
ATOM	3914	CA	ALA	B	374	12.249	22.111	54.936	1.00	23.10	B C
ATOM	3915	CB	ALA	B	374	12.423	20.733	55.580	1.00	26.30	B C
ATOM	3916	C	ALA	B	374	12.033	23.168	56.019	1.00	23.37	B C
ATOM	3917	O	ALA	B	374	10.916	23.353	56.496	1.00	23.95	B O
ATOM	3918	N	GLU	B	375	13.102	23.854	56.410	1.00	22.62	B N
ATOM	3919	CA	GLU	B	375	13.007	24.891	57.426	1.00	22.21	B C
ATOM	3920	CB	GLU	B	375	14.394	25.218	57.984	1.00	23.52	B C
ATOM	3921	CG	GLU	B	375	15.035	24.067	58.761	1.00	27.91	B C
ATOM	3922	CD	GLU	B	375	16.465	24.369	59.174	1.00	29.27	B C
ATOM	3923	OE1	GLU	B	375	16.666	25.158	60.120	1.00	31.60	B O
ATOM	3924	OE2	GLU	B	375	17.389	23.826	58.538	1.00	29.51	B O
ATOM	3925	C	GLU	B	375	12.380	26.139	56.823	1.00	22.31	B C
ATOM	3926	O	GLU	B	375	11.661	26.874	57.497	1.00	20.94	B O
ATOM	3927	N	VAL	B	376	12.664	26.376	55.545	1.00	21.78	B N
ATOM	3928	CA	VAL	B	376	12.106	27.526	54.840	1.00	21.13	B C
ATOM	3929	CB	VAL	B	376	12.666	27.613	53.394	1.00	18.71	B C
ATOM	3930	CG1	VAL	B	376	11.973	28.725	52.634	1.00	17.37	B C
ATOM	3931	CG2	VAL	B	376	14.176	27.854	53.429	1.00	15.43	B C
ATOM	3932	C	VAL	B	376	10.582	27.378	54.777	1.00	22.45	B C
ATOM	3933	O	VAL	B	376	9.841	28.336	55.006	1.00	22.60	B O
ATOM	3934	N	LEU	B	377	10.133	26.163	54.478	1.00	22.30	B N
ATOM	3935	CA	LEU	B	377	8.715	25.857	54.366	1.00	26.34	B C
ATOM	3936	CB	LEU	B	377	8.533	24.449	53.785	1.00	26.41	B C
ATOM	3937	CG	LEU	B	377	9.025	24.299	52.343	1.00	27.84	B C
ATOM	3938	CD1	LEU	B	377	9.044	22.837	51.924	1.00	27.54	B C
ATOM	3939	CD2	LEU	B	377	8.115	25.105	51.431	1.00	26.87	B C
ATOM	3940	C	LEU	B	377	7.976	25.971	55.693	1.00	27.31	B C
ATOM	3941	O	LEU	B	377	6.752	25.965	55.719	1.00	28.00	B O
ATOM	3942	N	GLU	B	378	8.722	26.069	56.788	1.00	27.51	B N
ATOM	3943	CA	GLU	B	378	8.126	26.189	58.113	1.00	28.70	B C
ATOM	3944	CB	GLU	B	378	8.796	25.221	59.100	1.00	33.15	B C
ATOM	3945	CG	GLU	B	378	8.265	23.796	59.082	1.00	39.47	B C
ATOM	3946	CD	GLU	B	378	9.030	22.878	60.036	1.00	44.38	B C
ATOM	3947	OE1	GLU	B	378	8.545	21.758	60.311	1.00	47.53	B O
ATOM	3948	OE2	GLU	B	378	10.119	23.271	60.506	1.00	44.23	B O
ATOM	3949	C	GLU	B	378	8.252	27.601	58.659	1.00	26.28	B C
ATOM	3950	O	GLU	B	378	7.780	27.886	59.752	1.00	26.40	B O
ATOM	3951	N	HIS	B	379	8.891	28.491	57.915	1.00	23.55	B N
ATOM	3952	CA	HIS	B	379	9.045	29.852	58.405	1.00	22.18	B C
ATOM	3953	CB	HIS	B	379	9.891	30.671	57.438	1.00	18.53	B C
ATOM	3954	CG	HIS	B	379	10.310	31.999	57.984	1.00	20.37	B C
ATOM	3955	CD2	HIS	B	379	11.503	32.430	58.455	1.00	16.86	B C
ATOM	3956	ND1	HIS	B	379	9.437	33.058	58.121	1.00	18.83	B N
ATOM	3957	CE1	HIS	B	379	10.076	34.084	58.653	1.00	19.47	B C
ATOM	3958	NE2	HIS	B	379	11.330	33.729	58.864	1.00	20.07	B N
ATOM	3959	C	HIS	B	379	7.672	30.488	58.604	1.00	22.39	B C
ATOM	3960	O	HIS	B	379	6.784	30.339	57.760	1.00	24.30	B O
ATOM	3961	N	PRO	B	380	7.477	31.199	59.734	1.00	21.58	B N
ATOM	3962	CD	PRO	B	380	8.461	31.340	60.818	1.00	20.38	B C
ATOM	3963	CA	PRO	B	380	6.218	31.870	60.091	1.00	20.86	B C
ATOM	3964	CB	PRO	B	380	6.521	32.487	61.458	1.00	22.72	B C
ATOM	3965	CG	PRO	B	380	7.574	31.573	62.013	1.00	23.24	B C
ATOM	3966	C	PRO	B	380	5.697	32.910	59.095	1.00	21.33	B C
ATOM	3967	O	PRO	B	380	4.483	33.127	59.013	1.00	17.95	B O
ATOM	3968	N	TRP	B	381	6.599	33.560	58.355	1.00	19.60	B N
ATOM	3969	CA	TRP	B	381	6.183	34.555	57.365	1.00	19.09	B C
ATOM	3970	CB	TRP	B	381	7.373	35.392	56.893	1.00	19.18	B C
ATOM	3971	CG	TRP	B	381	7.000	36.467	55.892	1.00	20.21	B C
ATOM	3972	CD2	TRP	B	381	7.254	36.450	54.478	1.00	18.07	B C

ATOM	3973	CE2	TRP	B	381	6.688	37.629	53.935	1.00	18.87	B	C
ATOM	3974	CE3	TRP	B	381	7.901	35.554	53.619	1.00	19.02	B	C
ATOM	3975	CD1	TRP	B	381	6.316	37.630	56.142	1.00	18.93	B	C
ATOM	3976	NE1	TRP	B	381	6.126	38.331	54.970	1.00	16.23	B	N
ATOM	3977	CZ2	TRP	B	381	6.748	37.929	52.570	1.00	16.90	B	C
ATOM	3978	CZ3	TRP	B	381	7.962	35.855	52.251	1.00	18.05	B	C
ATOM	3979	CH2	TRP	B	381	7.386	37.034	51.747	1.00	17.42	B	C
ATOM	3980	C	TRP	B	381	5.572	33.809	56.171	1.00	20.19	B	C
ATOM	3981	O	TRP	B	381	4.562	34.233	55.600	1.00	16.91	B	O
ATOM	3982	N	ILE	B	382	6.199	32.699	55.801	1.00	18.76	B	N
ATOM	3983	CA	ILE	B	382	5.719	31.887	54.695	1.00	22.56	B	C
ATOM	3984	CB	ILE	B	382	6.766	30.844	54.318	1.00	22.31	B	C
ATOM	3985	CG2	ILE	B	382	6.139	29.747	53.486	1.00	22.37	B	C
ATOM	3986	CG1	ILE	B	382	7.908	31.529	53.573	1.00	23.31	B	C
ATOM	3987	CD1	ILE	B	382	9.066	30.636	53.321	1.00	29.66	B	C
ATOM	3988	C	ILE	B	382	4.395	31.181	55.019	1.00	24.58	B	C
ATOM	3989	O	ILE	B	382	3.447	31.210	54.230	1.00	23.86	B	O
ATOM	3990	N	THR	B	383	4.348	30.543	56.183	1.00	25.64	B	N
ATOM	3991	CA	THR	B	383	3.167	29.825	56.640	1.00	25.76	B	C
ATOM	3992	CB	THR	B	383	3.462	29.123	57.982	1.00	25.87	B	C
ATOM	3993	OG1	THR	B	383	4.162	27.896	57.732	1.00	31.20	B	O
ATOM	3994	CG2	THR	B	383	2.196	28.841	58.734	1.00	28.47	B	C
ATOM	3995	C	THR	B	383	1.966	30.746	56.812	1.00	26.92	B	C
ATOM	3996	O	THR	B	383	0.817	30.336	56.615	1.00	27.54	B	O
ATOM	3997	N	ALA	B	384	2.234	31.994	57.175	1.00	26.10	B	N
ATOM	3998	CA	ALA	B	384	1.170	32.961	57.396	1.00	27.17	B	C
ATOM	3999	CB	ALA	B	384	1.653	34.053	58.326	1.00	25.11	B	C
ATOM	4000	C	ALA	B	384	0.635	33.584	56.119	1.00	28.32	B	C
ATOM	4001	O	ALA	B	384	-0.550	33.900	56.022	1.00	27.86	B	O
ATOM	4002	N	ASN	B	385	1.503	33.756	55.134	1.00	29.11	B	N
ATOM	4003	CA	ASN	B	385	1.090	34.392	53.898	1.00	32.57	B	C
ATOM	4004	CB	ASN	B	385	2.128	35.451	53.541	1.00	27.65	B	C
ATOM	4005	CG	ASN	B	385	2.247	36.512	54.625	1.00	26.99	B	C
ATOM	4006	OD1	ASN	B	385	1.328	37.303	54.829	1.00	25.20	B	O
ATOM	4007	ND2	ASN	B	385	3.367	36.517	55.342	1.00	23.02	B	N
ATOM	4008	C	ASN	B	385	0.807	33.447	52.735	1.00	35.05	B	C
ATOM	4009	O	ASN	B	385	0.812	33.859	51.580	1.00	35.34	B	O
ATOM	4010	N	SER	B	386	0.527	32.190	53.078	1.00	40.53	B	N
ATOM	4011	CA	SER	B	386	0.201	31.117	52.138	1.00	44.93	B	C
ATOM	4012	CB	SER	B	386	-0.537	31.661	50.910	1.00	45.41	B	C
ATOM	4013	OG	SER	B	386	-0.956	30.611	50.055	1.00	45.89	B	O
ATOM	4014	C	SER	B	386	1.436	30.343	51.701	1.00	48.13	B	C
ATOM	4015	O	SER	B	386	2.357	30.904	51.108	1.00	48.75	B	O
ATOM	4016	N	SER	B	387	1.435	29.046	52.006	1.00	51.11	B	N
ATOM	4017	CA	SER	B	387	2.536	28.143	51.673	1.00	52.94	B	C
ATOM	4018	CB	SER	B	387	3.430	27.924	52.898	1.00	52.84	B	C
ATOM	4019	OG	SER	B	387	4.439	26.960	52.630	1.00	53.68	B	O
ATOM	4020	C	SER	B	387	2.022	26.788	51.181	1.00	53.55	B	C
ATOM	4021	O	SER	B	387	2.221	25.788	51.903	1.00	56.01	B	O
ATOM	4022	OXT	SER	B	387	1.426	26.735	50.087	1.00	52.55	B	O
TER	4023		SER	B	387							
ATOM	4024	C1	FRA	Z	1	21.364	83.849	79.751	1.00	28.06	Z	C
ATOM	4025	C2	FRA	Z	1	21.204	82.482	80.488	1.00	28.48	Z	C
ATOM	4026	C3	FRA	Z	1	20.089	81.594	79.848	1.00	28.20	Z	C
ATOM	4027	C4	FRA	Z	1	20.171	81.530	78.286	1.00	29.96	Z	C
ATOM	4028	C5	FRA	Z	1	20.403	82.931	77.637	1.00	26.40	Z	C
ATOM	4029	N6	FRA	Z	1	21.562	83.678	78.268	1.00	26.70	Z	N
ATOM	4030	C7	FRA	Z	1	21.844	85.007	77.590	1.00	26.79	Z	C
ATOM	4031	C8	FRA	Z	1	22.091	84.946	76.062	1.00	22.84	Z	C
ATOM	4032	C9	FRA	Z	1	21.703	86.217	75.301	1.00	22.28	Z	C
ATOM	4033	O10	FRA	Z	1	22.186	86.127	73.930	1.00	21.29	Z	O
ATOM	4034	C11	FRA	Z	1	22.294	87.227	73.066	1.00	20.50	Z	C
ATOM	4035	C12	FRA	Z	1	22.781	87.073	71.728	1.00	19.83	Z	C
ATOM	4036	C13	FRA	Z	1	22.881	88.197	70.870	1.00	17.71	Z	C
ATOM	4037	C14	FRA	Z	1	22.506	89.483	71.312	1.00	15.27	Z	C
ATOM	4038	C15	FRA	Z	1	22.005	89.651	72.695	1.00	16.51	Z	C
ATOM	4039	C16	FRA	Z	1	21.911	88.516	73.537	1.00	18.78	Z	C
ATOM	4040	N17	FRA	Z	1	21.634	90.872	73.162	1.00	18.92	Z	N
ATOM	4041	C18	FRA	Z	1	21.733	91.911	72.347	1.00	15.67	Z	C
ATOM	4042	N19	FRA	Z	1	22.169	91.877	71.088	1.00	16.81	Z	N
ATOM	4043	C20	FRA	Z	1	22.560	90.693	70.539	1.00	16.78	Z	C
ATOM	4044	N21	FRA	Z	1	23.025	90.704	69.148	1.00	16.94	Z	N

	ATOM	4045	C22	FRA	Z	1	23.001	91.757	68.180	1.00	18.96	Z C
	ATOM	4046	C23	FRA	Z	1	24.061	91.923	67.246	1.00	17.20	Z C
	ATOM	4047	N24	FRA	Z	1	24.042	92.933	66.367	1.00	19.55	Z N
	ATOM	4048	C25	FRA	Z	1	22.992	93.783	66.394	1.00	18.00	Z C
5	ATOM	4049	N26	FRA	Z	1	21.955	93.708	67.214	1.00	17.17	Z N
	ATOM	4050	C27	FRA	Z	1	21.936	92.724	68.097	1.00	18.78	Z C
	ATOM	4051	N28	FRA	Z	1	23.043	94.876	65.467	1.00	22.15	Z N
	ATOM	4052	C29	FRA	Z	1	23.696	95.214	64.346	1.00	20.72	Z C
	ATOM	4053	C30	FRA	Z	1	23.352	96.585	63.786	1.00	19.36	Z C
10	ATOM	4054	C31	FRA	Z	1	22.405	97.470	64.411	1.00	17.69	Z C
	ATOM	4055	C32	FRA	Z	1	22.122	98.742	63.860	1.00	20.12	Z C
	ATOM	4056	C33	FRA	Z	1	22.776	99.153	62.676	1.00	17.24	Z C
	ATOM	4057	C34	FRA	Z	1	23.710	98.303	62.042	1.00	17.77	Z C
	ATOM	4058	C35	FRA	Z	1	23.998	97.035	62.589	1.00	17.80	Z C
15	ATOM	4059	O36	FRA	Z	1	24.531	94.448	63.824	1.00	21.83	Z O
	ATOM	4060	O37	FRA	Z	1	23.170	85.827	71.240	1.00	20.79	Z O
	ATOM	4061	C38	FRA	Z	1	22.679	85.375	69.951	1.00	26.55	Z C
	ATOM	4062	O39	FRA	Z	1	23.466	84.677	75.820	1.00	24.51	Z O
	TER	4063		FRA	Z	1						
20	ATOM	4064	C1	FRA	Y	1	1.515	35.986	27.679	1.00	36.52	Y C
	ATOM	4065	C2	FRA	Y	1	0.608	36.976	26.867	1.00	37.59	Y C
	ATOM	4066	C3	FRA	Y	1	-0.401	36.230	25.961	1.00	36.15	Y C
	ATOM	4067	C4	FRA	Y	1	0.319	35.193	25.054	1.00	37.83	Y C
	ATOM	4068	C5	FRA	Y	1	1.177	34.183	25.879	1.00	36.12	Y C
25	ATOM	4069	N6	FRA	Y	1	2.132	34.827	26.897	1.00	36.16	Y N
	ATOM	4070	C7	FRA	Y	1	3.479	35.234	26.297	1.00	37.30	Y C
	ATOM	4071	C8	FRA	Y	1	4.332	34.189	25.489	1.00	32.04	Y C
	ATOM	4072	C9	FRA	Y	1	4.647	32.852	26.202	1.00	29.29	Y C
	ATOM	4073	O10	FRA	Y	1	6.097	32.795	26.275	1.00	25.58	Y O
30	ATOM	4074	C11	FRA	Y	1	6.903	31.673	26.442	1.00	20.22	Y C
	ATOM	4075	C12	FRA	Y	1	8.327	31.834	26.469	1.00	19.90	Y C
	ATOM	4076	C13	FRA	Y	1	9.170	30.706	26.629	1.00	18.27	Y C
	ATOM	4077	C14	FRA	Y	1	8.622	29.412	26.769	1.00	16.62	Y C
	ATOM	4078	C15	FRA	Y	1	7.143	29.247	26.749	1.00	16.07	Y C
35	ATOM	4079	C16	FRA	Y	1	6.320	30.391	26.580	1.00	17.70	Y C
	ATOM	4080	N17	FRA	Y	1	6.583	28.029	26.887	1.00	17.71	Y N
	ATOM	4081	C18	FRA	Y	1	7.389	26.981	27.040	1.00	17.21	Y C
	ATOM	4082	N19	FRA	Y	1	8.725	27.007	27.067	1.00	17.12	Y N
	ATOM	4083	C20	FRA	Y	1	9.371	28.193	26.934	1.00	17.89	Y C
40	ATOM	4084	N21	FRA	Y	1	10.845	28.199	26.966	1.00	19.44	Y N
	ATOM	4085	C22	FRA	Y	1	11.804	27.160	27.225	1.00	17.92	Y C
	ATOM	4086	C23	FRA	Y	1	13.046	27.089	26.514	1.00	17.84	Y C
	ATOM	4087	N24	FRA	Y	1	13.927	26.091	26.750	1.00	17.67	Y N
	ATOM	4088	C25	FRA	Y	1	13.591	25.172	27.677	1.00	19.86	Y C
45	ATOM	4089	N26	FRA	Y	1	12.465	25.164	28.390	1.00	22.22	Y N
	ATOM	4090	C27	FRA	Y	1	11.584	26.130	28.180	1.00	20.19	Y C
	ATOM	4091	N28	FRA	Y	1	14.520	24.102	27.878	1.00	21.17	Y N
	ATOM	4092	C29	FRA	Y	1	15.769	23.800	27.502	1.00	20.01	Y C
	ATOM	4093	C30	FRA	Y	1	16.310	22.465	27.980	1.00	19.29	Y C
50	ATOM	4094	C31	FRA	Y	1	15.545	21.551	28.783	1.00	19.61	Y C
	ATOM	4095	C32	FRA	Y	1	16.081	20.315	29.195	1.00	21.23	Y C
	ATOM	4096	C33	FRA	Y	1	17.394	19.964	28.819	1.00	18.14	Y C
	ATOM	4097	C34	FRA	Y	1	18.172	20.843	28.033	1.00	19.61	Y C
	ATOM	4098	C35	FRA	Y	1	17.642	22.083	27.612	1.00	19.21	Y C
55	ATOM	4099	O36	FRA	Y	1	16.421	24.575	26.797	1.00	19.90	Y O
	ATOM	4100	O37	FRA	Y	1	8.904	33.109	26.339	1.00	21.63	Y O
	ATOM	4101	C38	FRA	Y	1	10.186	33.273	25.678	1.00	23.16	Y C
	ATOM	4102	O39	FRA	Y	1	3.746	33.908	24.230	1.00	36.52	Y O
60	TER	4103		FRA	Y	1						
	ATOM	4104	O	HOH	E	1	-2.816	80.929	50.812	1.00	19.03	E O
	ATOM	4105	O	HOH	E	2	3.978	72.365	54.056	1.00	19.03	E O
	ATOM	4106	O	HOH	E	3	13.505	98.252	72.880	1.00	19.36	E O
	ATOM	4107	O	HOH	E	4	28.293	104.582	83.681	1.00	21.47	E O
65	ATOM	4108	O	HOH	E	6	6.360	44.178	47.881	1.00	23.42	E O
	ATOM	4109	O	HOH	E	7	1.770	73.865	68.162	1.00	20.46	E O
	ATOM	4110	O	HOH	E	8	8.297	17.524	35.431	1.00	28.17	E O
	ATOM	4111	O	HOH	E	9	4.373	82.422	53.549	1.00	66.83	E O
	ATOM	4112	O	HOH	E	10	9.876	77.587	53.891	1.00	15.33	E O
70	ATOM	4113	O	HOH	E	11	13.114	23.318	30.599	1.00	23.68	E O
	ATOM	4114	O	HOH	E	12	7.067	14.767	42.081	1.00	41.33	E O
	ATOM	4115	O	HOH	E	13	15.665	28.507	29.364	1.00	35.38	E O

ATOM	4116	O	HOH	E	14	8.724	81.834	51.911	1.00	15.54	E	O
ATOM	4117	O	HOH	E	15	21.092	27.236	30.877	1.00	29.72	E	O
ATOM	4118	O	HOH	E	16	4.235	23.958	10.152	1.00	18.27	E	O
ATOM	4119	O	HOH	E	17	21.990	41.088	42.974	1.00	32.56	E	O
ATOM	4120	O	HOH	E	18	20.666	46.477	48.657	1.00	22.11	E	O
ATOM	4121	O	HOH	E	19	12.394	30.572	26.200	1.00	25.85	E	O
ATOM	4122	O	HOH	E	20	24.458	88.275	67.914	1.00	18.95	E	O
ATOM	4123	O	HOH	E	21	16.023	94.041	76.489	1.00	18.64	E	O
ATOM	4124	O	HOH	E	22	-3.046	75.441	65.884	1.00	19.92	E	O
ATOM	4125	O	HOH	E	24	13.742	101.239	70.093	1.00	20.42	E	O
ATOM	4126	O	HOH	E	25	2.139	79.403	76.859	1.00	24.59	E	O
ATOM	4127	O	HOH	E	26	-0.923	97.738	56.694	1.00	26.97	E	O
ATOM	4128	O	HOH	E	27	27.493	25.824	48.659	1.00	25.58	E	O
ATOM	4129	O	HOH	E	28	-3.060	85.100	45.284	1.00	28.40	E	O
ATOM	4130	O	HOH	E	29	2.126	21.471	26.630	1.00	18.24	E	O
ATOM	4131	O	HOH	E	30	19.055	98.237	66.551	1.00	26.93	E	O
ATOM	4132	O	HOH	E	31	5.015	20.070	34.897	1.00	27.21	E	O
ATOM	4133	O	HOH	E	32	20.699	97.163	78.060	1.00	20.06	E	O
ATOM	4134	O	HOH	E	33	19.905	95.504	66.214	1.00	16.74	E	O
ATOM	4135	O	HOH	E	34	26.799	36.524	56.357	1.00	23.12	E	O
ATOM	4136	O	HOH	E	35	7.281	42.459	52.886	1.00	27.29	E	O
ATOM	4137	O	HOH	E	36	-5.229	82.177	76.134	1.00	17.35	E	O
ATOM	4138	O	HOH	E	37	16.156	81.681	74.210	1.00	33.58	E	O
ATOM	4139	O	HOH	E	38	17.171	26.456	35.298	1.00	26.63	E	O
ATOM	4140	O	HOH	E	41	10.220	96.211	76.240	1.00	36.39	E	O
ATOM	4141	O	HOH	E	42	21.575	87.342	80.619	1.00	26.03	E	O
ATOM	4142	O	HOH	E	43	-2.344	82.211	46.311	1.00	33.39	E	O
ATOM	4143	O	HOH	E	44	1.411	102.153	63.920	1.00	40.99	E	O
ATOM	4144	O	HOH	E	45	22.412	37.472	55.894	1.00	36.08	E	O
ATOM	4145	O	HOH	E	46	2.300	24.457	31.665	1.00	23.22	E	O
ATOM	4146	O	HOH	E	47	13.621	22.599	34.360	1.00	23.98	E	O
ATOM	4147	O	HOH	E	48	15.081	50.361	55.761	1.00	28.43	E	O
ATOM	4148	O	HOH	E	49	14.580	93.564	78.622	1.00	24.96	E	O
ATOM	4149	O	HOH	E	50	26.890	18.450	12.611	1.00	42.82	E	O
ATOM	4150	O	HOH	E	51	9.227	107.514	67.012	1.00	41.46	E	O
ATOM	4151	O	HOH	E	52	34.558	108.086	67.299	1.00	37.65	E	O
ATOM	4152	O	HOH	E	53	10.050	90.871	55.783	1.00	29.24	E	O
ATOM	4153	O	HOH	E	54	7.944	16.482	49.236	1.00	41.77	E	O
ATOM	4154	O	HOH	E	55	13.318	100.169	53.864	1.00	42.27	E	O
ATOM	4155	O	HOH	E	56	7.453	71.694	56.237	1.00	34.69	E	O
ATOM	4156	O	HOH	E	57	-0.370	31.293	25.399	1.00	22.63	E	O
ATOM	4157	O	HOH	E	58	6.282	69.233	70.952	1.00	40.32	E	O
ATOM	4158	O	HOH	E	59	16.826	72.690	51.895	1.00	39.22	E	O
ATOM	4159	O	HOH	E	60	26.960	20.330	32.431	1.00	46.00	E	O
ATOM	4160	O	HOH	E	61	24.484	34.166	17.080	1.00	57.71	E	O
ATOM	4161	O	HOH	E	62	15.070	29.732	24.722	1.00	36.63	E	O
ATOM	4162	O	HOH	E	63	2.410	82.045	76.883	1.00	31.15	E	O
ATOM	4163	O	HOH	E	64	20.509	17.863	8.881	1.00	34.06	E	O
ATOM	4164	O	HOH	E	65	9.108	18.512	47.676	1.00	36.58	E	O
ATOM	4165	O	HOH	E	66	-4.442	94.264	72.560	1.00	35.02	E	O
ATOM	4166	O	HOH	E	67	4.615	73.935	73.283	1.00	34.26	E	O
ATOM	4167	O	HOH	E	68	20.674	96.637	81.076	1.00	32.24	E	O
ATOM	4168	O	HOH	E	69	6.012	84.836	76.526	1.00	39.65	E	O
ATOM	4169	O	HOH	E	70	18.931	64.756	50.070	1.00	41.17	E	O
ATOM	4170	O	HOH	E	71	1.034	33.236	39.187	1.00	32.26	E	O
ATOM	4171	O	HOH	E	72	-3.531	21.419	23.837	1.00	33.17	E	O
ATOM	4172	O	HOH	E	73	35.386	104.215	87.572	1.00	48.96	E	O
ATOM	4173	O	HOH	E	74	17.897	25.522	63.076	1.00	45.88	E	O
ATOM	4174	O	HOH	E	75	21.283	17.561	47.461	1.00	37.66	E	O
ATOM	4175	O	HOH	E	76	-11.086	90.035	66.851	1.00	30.87	E	O
ATOM	4176	O	HOH	E	77	11.320	20.363	58.814	1.00	46.67	E	O
ATOM	4177	O	HOH	E	78	-6.338	85.994	41.967	1.00	51.31	E	O
ATOM	4178	O	HOH	E	79	3.655	87.067	43.145	1.00	39.38	E	O
ATOM	4179	O	HOH	E	81	7.253	86.756	37.906	1.00	59.51	E	O
ATOM	4180	O	HOH	E	82	23.816	46.171	47.749	1.00	28.26	E	O
ATOM	4181	O	HOH	E	83	-2.313	31.734	47.707	1.00	41.05	E	O
ATOM	4182	O	HOH	E	84	11.459	17.532	33.022	1.00	35.50	E	O
ATOM	4183	O	HOH	E	85	1.163	30.110	41.773	1.00	28.95	E	O
ATOM	4184	O	HOH	E	86	6.404	108.929	60.380	1.00	44.61	E	O
ATOM	4185	O	HOH	E	87	6.970	44.481	59.964	1.00	33.00	E	O
ATOM	4186	O	HOH	E	88	6.136	40.362	59.850	1.00	35.96	E	O
ATOM	4187	O	HOH	E	89	8.854	36.982	12.914	1.00	51.29	E	O

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ATOM   4188  O   HOH E  90      14.894  17.557  10.137  1.00 29.07      E   O
ATOM   4189  O   HOH E  91       3.598  70.913  41.429  1.00 37.85      E   O
ATOM   4190  O   HOH E  92      15.660  96.593  64.706  1.00 34.79      E   O
ATOM   4191  O   HOH E  93      -1.289  22.000  25.700  1.00 53.85      E   O
ATOM   4192  O   HOH E  94      18.658  94.873  78.816  1.00 34.79      E   O
ATOM   4193  O   HOH E  95      24.030  37.111  44.167  1.00 31.33      E   O
ATOM   4194  O   HOH E  96      24.327 108.825  70.586  1.00 43.44      E   O
ATOM   4195  O   HOH E  97      17.453  29.940  39.065  1.00 62.04      E   O
ATOM   4196  O   HOH E  98     -10.095  77.380  58.416  1.00 32.83      E   O
ATOM   4197  O   HOH E  99       1.372  41.175  43.439  1.00 30.57      E   O
ATOM   4198  O   HOH E 100      13.220  40.977  61.050  1.00 25.13      E   O
ATOM   4199  O   HOH E 101      20.635  23.766  29.311  1.00 36.67      E   O
ATOM   4200  O   HOH E 102       6.907 103.740  69.211  1.00 39.48      E   O
ATOM   4201  O   HOH E 103      29.965  20.328  27.392  1.00 35.16      E   O
ATOM   4202  O   HOH E 104      -5.202  80.206  74.097  1.00 29.87      E   O
ATOM   4203  O   HOH E 105      -0.936  62.297  61.894  1.00 42.93      E   O
ATOM   4204  O   HOH E 106      36.982 102.874  54.415  1.00 36.76      E   O
ATOM   4205  O   HOH E 107       5.889 102.017  53.094  1.00 63.79      E   O
ATOM   4206  O   HOH E 108      39.219  43.505  52.395  1.00 38.65      E   O
TER    4207      HOH E 108
END
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The shape of the ATP binding pocket is defined by the atomic coordinates of the atoms in the amino-acid residues in Tables 1 and 2. Table 1 lists the atomic coordinates for [T287D] Aurora A(122-396) catalytic domain, together with the AMP-PNP molecule, in Protein Data Bank (PDB) format, as determined from the first crystalline form. Table 2-lists the atomic coordinates for the two independent molecules of the GSHM-[T287D]Aurora A (122-400) catalytic domain, together with the inhibitor of formula II, in PDB format, as determined from the second crystalline form. The atomic coordinates are listed in those lines that begin with the code ATOM or HETATM, one atom per line. Following the code are: the unique atom number; the atom name; the amino acid residue name; the protein chain identifier; the amino acid residue number; the atomic coordinates x, y, and z in orthogonal Angstrom space; the atomic occupancy factor; the atomic temperature factor; the chain identifier; and the atom type. The atomic coordinates of the ATP analogue AMP-PNP carry the residue name of-ANP. Solvent water molecules carry the residue name of HOH, and a citrate and a bound phosphate derived from the crystallisation buffer carry the residue name of FRA. In the inhibitor complex the inhibitor molecules carry the residue name of FRA.

It is possible to reproduce the shape of the [T287D]Aurora A active site binding pocket through carrying out similar structure determinations with minor variations in the experimental conditions (including variations in construct such as mutants, variants and homologues, variations in crystallisation conditions, crystal form, trial model used in molecular replacement, etc.). Different experiments may give rise to apparently different co-ordinates, but those in the art will realise that two apparently different sets of coordinates for the same or similar proteins can be shown to be equivalent by superposition of the molecules. For example, the coordinates in Tables 1 and 2 are different numerically. But following superposition they can be seen to describe the same molecule. It will be appreciated that, according to accepted practice, the atomic coordinates may vary within certain limits due to experimental variation. Such variation includes standard experimental error (coordinates determined for the same construct may vary somewhat, for example within 0.3 Å) and other variation (for example, coordinates of Aurora mutants, variants, or homologues). The co-ordinates of the active site ATP binding site may also differ upon introduction of a different small molecule inhibitor, where flexible portions of the binding site adopt a new conformation specific to a type of inhibitor. For example, following superposition, the protein coordinates in Table 1 are seen to be marginally different to those in Table 2, as a result of flexible portions of the protein being influenced by the presence of a different inhibitor. This constitutes a

modification of the active site ATP binding site rather than the creation of a new site. Those in the art will realise that kinases in general have flexible active sites, and adopt a number of biologically relevant conformations related to the state of catalytic activation. Therefore, for the purposes of differentiating the shape of the active site ATP-binding pocket from that in other kinases, the binding pocket is best defined by a subset of amino acids that are least affected by flexible protein responses to inhibitor binding. Thus, a protein can be said to have the Aurora active site described here if, following superposition, the positions of all atoms in the active site residues in set B, i.e. Arg136, Leu138, Gly139, Val146, Ala159, Lys161, Leu163, Ile183, Gln184, Leu193, Leu195, Leu207, Leu209, Glu210, Tyr211, Ala212, Pro213, Leu214, Gly215, Thr216, Arg219, Glu259, Asn260 and Leu262 or their equivalents, are within a root mean square deviation of 1.0 Å of the coordinates of these amino acid residues given in Tables 1 and 2. An equivalent residue is an amino acid residue in any Aurora mutant, variant, or homologue that occurs at one of the amino acid sequence positions in Tables 1 or 2 – if the residue is not identical, only the N, Cα, Cβ, C, O atoms may be sensibly included in the rmsd calculation. It is also understood that if equivalent residues are not present in a particular variant or homologue, then they are omitted from the calculation of the average distance.

The criterion of 1.0 Å is intended to be large enough to allow the types of variations described above, yet small enough to discriminate between the active sites of Aurora kinases and other kinases. That this criterion is reasonable is illustrated in Table 3, which compares [T287D]Aurora A to one of the most closely related kinases, PKA.

			1atp	**1l3r**	**1bx6**	**1apm**	**1ydt**	**1cmk**
1 - 2	0.85	**1-PKA**	1.32	1.32	1.29	1.24	1.28	1.17
1 - 3	0.67	**2-PKA**	1.19	1.14	1.08	1.13	1.13	1.13
2 - 3	0.42	**3-PKA**	1.14	1.08	1.09	1.08	1.10	1.21

Table 3: rms deviations in Å between all atoms of set B amino acids in the active site.

The top row refers to the PDB codes for 6 entries of a different kinase, protein kinase A (PKA). The bold numbers refer to the Tables 1 and 2 which contain Aurora coordinates. Thus, when independent structure determinations of Aurora are compared (1-2, 1-3, 2-3) the rmsd is

less than 1 Å, whereas when Aurora is compared to PKA (6 independent structures) the rmsd is greater than 1 Å.

Thus, according to a further aspect of the invention, we provide the shape of the active site ATP binding pocket in Aurora protein kinase as defined by the atomic coordinates given in Tables 1 and 2 or by equivalent coordinates. Equivalent coordinates are those for which the subset of least flexible residues (set B) have atomic positions on average within 1.0 Å of those in the Aurora active site ATP binding pocket as defined by the coordinates in Tables 1 and 2.

According to a further aspect of the invention we provide a method to determine or design the three-dimensional structure of a crystal form of Aurora (including Aurora A homologues, variants, mutants, and inhibitor complexes) by using a particular Aurora A catalytic domain structure. The atomic co-ordinates of an Aurora A crystal may be used to model the structure of a second Aurora crystal by difference Fourier or molecular replacement methods.

The crystal structure of the Aurora A kinase catalytic domain described herein can be used to model the three-dimensional structures of other Aurora kinases. Furthermore, alternative methods of determining three-dimensional structure that do not rely on X-ray diffraction techniques and thus do not require crystallization of the protein, such as NMR techniques, are simplified if a model of the structure is available for refinement using the additional data gathered by the alternative technique. Thus, definition of the three-dimensional structure of the catalytic domain of Aurora A kinase enables one of skill in the art to determine the structure of the catalytic domains of other Aurora kinases.

Knowledge of the three-dimensional structure of the catalytic domain of Aurora A kinase provides a means for investigating the mechanism of action of the protein and tools for identifying inhibitors of its function. Knowledge of the three-dimensional structure of the catalytic domain of Aurora A kinase allows one to design molecules capable of binding thereto, including molecules which are capable of inhibiting (partially or completely) the activity of Aurora A kinase.

Illustrative crystalline forms of polypeptides of this invention having various physicochemical characteristics are disclosed herein. Preferred crystalline forms invention are capable of diffracting x-rays to a resolution of better than about 3.5 Å, and more preferably to a resolution of 3.0 Å or better, and even more preferably to a resolution of 2.2 Å or better, and are useful for determining the three-dimensional structure of the material.

Crystalline compositions of this invention specifically include those in which the crystals comprise Aurora kinase family proteins characterized by the structural coordinates set forth in any of the accompanying tables or characterized by coordinates having a root mean square deviation therefrom, with respect to backbone atoms of amino acids given in the Tables, of 1.5 Å or less. Crystalline compositions of this invention also include those in which the crystals comprise Aurora kinase family proteins characterized by having a binding site defined by the x,y,z-coordinates of atoms in the set of amino acid residues (set A) given by the list Arg136, Leu138, Gly139, Lys140, Gly141, Val146, Lys161, Leu163, Val177, Glu180, Val181, Ile183, Gln184, Leu193, Leu195, Leu207, Leu209, Glu210, Tyr211, Ala212, Pro213, Leu214, Gly215, Thr216, Arg219, Glu259, Asn260, Leu262, Ala272, Asp273, Phe274, Gly275, Trp276, Ser277, Val278, and His279, the atomic coordinates being listed in Tables 1 and 2. Further, crystalline forms of polypeptides of this invention also include those in which the crystals comprise Aurora kinase family proteins in which the binding site is defined by the x,y,z-coordinates of atoms in the set of amino acid residues (set B) given by the list Arg136, Leu138, Gly139, Val1146, Ala159, Lys161, Leu163, Ile183, Gln184, Leu193, Leu195, Leu207, Leu209, Glu210, Tyr211, Ala212, Pro213, Leu214, Gly215, Thr216, Arg219, Glu259, Asn260 and Leu262 or their equivalent, are within a root mean square deviation of 1.0 Å of the coordinates of these amino acid residues given in Tables 1 and 2.

Structural coordinates of a crystalline composition of this invention may be stored in a machine-readable form on a machine-readable storage medium, such as a computer hard drive, diskette, DAT tape, for display as a three-dimensional shape or for other uses involving computer-assisted manipulation of, or computation based on, the structural coordinates or the three-dimensional structures they define. For example, data defining the three dimensional structure of a protein of the Aurora kinase family, or portions or structurally similar homologues of such proteins, may be stored in a machine-readable storage medium and displayed as a three-dimensional representation of the protein structure, typically using a computer capable of reading the data from said storage medium and programmed with instructions for creating the representation from such data. This invention thus encompasses a machine, such as a computer, having a memory which contains data representing the structural coordinates of a crystalline composition of this invention, such as the coordinates set forth in Tables 1 and 2, together with additional optional data and instructions for manipulating such data. Such data may be used for a variety of purposes, such as the elucidation of other related structures and drug discovery.

For example, a first set of such machine readable data may be combined with a second set of machine-readable data using a machine programmed with instructions for using the first data set and the second data set to determine at least a portion of the coordinates corresponding to the second set of machine-readable data. For instance, the first set of data may comprise a Fourier transform of at least a portion of the coordinates for Aurora kinase proteins set forth in Tables 1 and 2, while the second data set may comprise X-ray diffraction data of a molecule or molecular complex.

More specifically, one of the objects of this invention is to provide three-dimensional structural information on new complexes of Aurora kinase family members (e.g., complexed with an ATP analogue or an inhibitor, such as a synthetic inhibitor), new Aurora kinase family members and variants of any of the foregoing. The structural coordinates of a crystalline composition of this invention, or portions thereof, can be used to solve, e.g. by molecular replacement, the three dimensional structure of a crystalline form of such a polypeptide or polypeptide complex. Doing so involves obtaining x-ray diffraction data for crystals of the polypeptide or polypeptide complex (e.g., in complex with an ATP analogue or an inhibitor, such as a synthetic inhibitor) for which one wishes to determine the three dimensional structure. The three-dimensional structure of that polypeptide or complex is determined by analyzing the x-ray diffraction data using molecular replacement techniques with reference to the structural coordinates provided. For example, molecular replacement can use a molecule having a known structure as a starting point to model the structure of an unknown crystalline sample. This technique is based on the principle that two molecules which have similar structures, orientations and positions in the unit cell diffract similarly. The term "molecular replacement" refers to a method that involves generating a preliminary model of a crystal whose atomic coordinates are not known, by orienting and positioning a related molecule whose atomic coordinates are known. Phases are then calculated from this model and combined with observed amplitudes to give an approximate Fourier synthesis of the structure whose coordinates are unknown. Molecular replacement involves positioning the known structure in the unit cell in the same location and orientation as the unknown structure. Once positioned, the atoms of the known structure in the unit cell are used to calculate the structure factors that would result from a hypothetical diffraction experiment. This involves rotating the known structure in the six dimensions (three angular and three spatial dimensions) until alignment of the known structure with the experimental data is achieved. This approximate structure can be refined to yield a more accurate and often higher resolution structure using

various refinement techniques. For instance, the resultant model for the structure defined by the experimental data may be subjected to rigid body refinement in which the model is subjected to limited additional rotation in the six dimensions yielding positioning shifts of under about 5%. The refined model may then be further refined using other known refinement methods.

For example, one may use molecular replacement to exploit a set of coordinates such as set forth in Table 1 or Table 2 to determine the structure of the catalytic domain of Aurora kinase in complex with other than ATP-PNP or the inhibitor of formula II.

The present invention also relates to designing and, optionally producing, a homologue of Aurora kinase, such as a homologue of Aurora kinase A, that mimics the three-dimensional structure of the Aurora kinase. The method comprises:

(i) determining the three-dimensional coordinates of atoms of an Aurora kinase;

(ii) providing a computer having a memory means, a data input means, a visual display means, said memory means containing three-dimensional molecular simulation software operable to retrieve co-ordinate data from said memory means and to display a three-dimensional representation of a molecule on said visual display means and being operable to produce a modified three-dimensional homologue representation responsive to operator-selected changes to the structure of the Aurora kinase and to display the three-dimensional representation of the modified three-dimensional homologue;

(iii) inputting three-dimensional co-ordinate data of atoms of Aurora kinase into the computer and storing said data in the memory means;

(iv) inputting into the data input means of said computer at least one operator-selected change in structure of the Aurora kinase;

(v) executing said molecular simulation software to produce a modified three-dimensional molecular representation of the homologue structure;

(vi) displaying the three-dimensional representation of the homologue on said visual display means, whereby changes in three-dimensional structure of the Aurora kinase resulting from changes on structure can be visually monitored;

(vii) repeating steps (iv) through (vi) to produce a multiplicity of homologues; and

(viii) selecting a homologue structure represented by a three-dimensional representation wherein the three-dimensional configuration and spatial arrangements of the kinase catalytic domain remain substantially preserved,

thereby producing a homologue of Aurora kinase that mimics the three-dimensional structure of the Aurora kinase.

The present invention also relates to a method of producing a modulator of Aurora kinase (particularly inhibitors), such as a modulator of Aurora kinase A. The method comprises identifying a compound or molecule or designing a compound or molecule that fits into the active site ATP binding pocket of the Aurora kinase, wherein the ATP binding pocket is defined by (a) Arg136, Leu138, Gly139, Lys140, Gly141, Val146, Lys161, Leu163, Val177, Glu180, Val181, Ile183, Gln184, Leu193, Leu195, Leu207, Leu209, Glu210, Tyr211, Ala212, Pro213, Leu214, Gly215, Thr216, Arg219, Glu259, Asn260, Leu262, Ala272, Asp273, Phe274, Gly275, Trp276, Ser277, Val278, and His279, the atomic coordinates being listed in Tables 1 and 2 or (b) the x,y,z- coordinates of atoms in the set of amino acid residues (set B) given by the list Arg136, Leu138, Gly139, Val146, Ala159, Lys161, Leu163, Ile183, Gln184, Leu193, Leu195, Leu207, Leu209, Glu210, Tyr211, Ala212, Pro213, Leu214, Gly215, Thr216, Arg219, Glu259, Asn260 and Leu262, each having coordinates as described in Tables 1 and 2, thereby producing a modulator of Aurora kinase.

Another object of the invention is to provide a method for determining the three-dimensional structure of the catalytic domain of an Aurora kinase protein, or the catalytic domain of an Aurora kinase protein in complex with an inhibitor, using homology modeling techniques and structural coordinates for a composition of this invention. Homology modeling involves constructing a model of an unknown structure using structural coordinates of one or more related proteins, protein domains and/or subdomains. Homology modeling may be conducted by fitting common or homologous portions of the protein or peptide whose three dimensional structure is to be solved to the three dimensional structure of homologous structural elements. This approach can be used to rebuild part or all of a three dimensional structure with replacement of amino acids (or other components) by those of the related structure to be solved. For example, using the structural coordinates of the catalytic domain of an Aurora kinase in complex with AMP-PNP or the inhibitor of formula II, it is possible to determine the three dimensional structure of the catalytic domain of another Aurora kinase protein through the use of homology modeling. Those coordinates may be stored, displayed, manipulated and otherwise used in like fashion as the Aurora kinase coordinates of Tables 1-2.

Thus, crystalline compositions of this invention provide a starting material for use in solving the three-dimensional structure of other Aurora kinase polypeptides.

By way of further example, the structure defined by the machine readable data may be computationally evaluated for its ability to associate with various chemical entities. The term "chemical entity", as used herein, refers to chemical compounds, complexes of at least two chemical compounds, and fragments of such compounds or complexes.

For instance, a first set of machine-readable data defining the three-dimensional structure of an Aurora kinase family protein, or a portion or complex thereof, is combined with a second set of machine-readable data defining the structure of a chemical entity or moiety of interest using a machine programmed with instructions for evaluating the ability of the chemical entity or moiety to associate with the Aurora kinase family protein or portion or complex thereof and/or the location and/or orientation of such association. Such methods provide insight into the location, orientation and energetics of association of the Aurora kinase family protein with such chemical entities. Chemical entities that associate or interact with an Aurora kinase may inhibit its interaction with naturally occurring ligands for the protein and may inhibit biological functions mediated by such interaction. Such chemical entities are drug candidates.

The protein structure encoded by the data may be displayed in a graphical format permitting visual inspection of the structure, as well as visual inspection of the structure's association with chemical entities. Alternatively, more quantitative or computational methods may be used. For example, one method of this invention for evaluating the ability of a chemical entity to associate with any of the molecules or molecular complexes set forth herein comprises the steps of: a) employing computational means to perform a fitting operation between the chemical entity and a binding pocket or other surface feature of the molecule or molecular complex; and b) analyzing the results of the fitting operation to quantify the association between the chemical entity and the binding pocket.

This invention further provides for the use of the structural coordinates of a crystalline composition of this invention, or portions thereof, to identify reactive amino acids, such as cysteine residues, within the three-dimensional structure, such as within or adjacent to the catalytic domain; to generate and visualize a molecular surface, such as a water-accessible surface or a surface comprising the space-filling van der Waals surface of all atoms; to calculate and visualize the size and shape of surface features of the protein or complex, e.g., ligand binding pockets; to locate potential H-bond donors and acceptors within the three-dimensional structure, preferably within or adjacent to a ligand binding site; to calculate regions of hydrophobicity and hydrophilicity within the three-dimensional structure,

preferably within or adjacent to a ligand binding site; and to calculate and visualize regions on or adjacent to the protein surface of favorable interaction energies with respect to selected functional groups of interest (e.g. amino, hydroxyl, carboxyl, methylene, alkyl, alkenyl, aromatic carbon, aromatic rings, heteroaromatic rings, substituted and unsubstituted phosphates, substituted and unsubstituted phosphonates, substituted and unsubstituted fluoro and difluorophosphonates; etc.). One may use the foregoing approaches for characterizing the protein and its interactions with moieties of potential ligands to design or select compounds capable of specific covalent attachment to reactive amino acids (e.g., cysteine) and to design or select compounds of complementary characteristics (e.g., size, shape, charge, hydrophobicity/hydrophilicity, ability to participate in hydrogen bonding, etc.) to surface features of the protein, a set of which may be preselected. Using the structural coordinates, one may also predict or calculate the orientation, binding constant or relative affinity of a given ligand to the protein in the complexed state, and use that information to design or select compounds of improved affinity.

In such cases, the structural coordinates of the Aurora kinase family protein, or portion or complex thereof, are entered in machine readable form into a machine programmed with instructions for carrying out the desired operation and containing any necessary additional data (e.g. data defining structural and/or functional characteristics of a potential ligand or moiety thereof, defining molecular characteristics of the various amino acids).

One method of this invention provides for selecting from a database of chemical structures a molecular compound capable of binding to an Aurora kinase family protein (e.g., coordinates defining the three dimensional structure of an Aurora kinase family protein or a portion thereof). Points associated with the three dimensional structure (structural coordinates) of a crystalline form of Aurora A kinase catalytic domain are characterized with respect to the favorability of interactions with one or more functional groups. A database of chemical structures is then searched for candidate compounds containing one or more functional groups disposed for favorable interaction with the protein based on the prior characterization. Compounds having structures which best fit the points of favorable interaction with the three dimensional structure are thus identified.

It is often preferred, although not required, that such searching be conducted with the aid of a computer. In that case a first set of machine-readable data defining the three-dimensional structure of an Aurora kinase family protein, or a portion or complex thereof, is combined with a second set of machine readable data defining one or more moieties or

functional groups of interest, using a machine programmed with instructions for identifying preferred locations for favorable interaction between the functional group(s) and atoms of the protein. A third set of data, which defines the location(s) of favorable interaction between protein and functional group(s) is generated. The third set of data is then combined with a fourth set of data defining the three-dimensional structures of one or more chemical entities using a machine programmed with instructions for identifying chemical entities containing functional groups to best fit the locations of their respective favorable interaction with the protein.

Compounds of the structures selected or designed by any of the foregoing means may be tested for their ability to bind to an Aurora kinase family protein, inhibit the binding of an Aurora kinase family protein to a natural or non-natural ligand therefor, and/or inhibit a biological function mediated by an Aurora kinase family member.

The new crystal may be a crystal of a homologue, variant, mutant, or inhibitor complex of Aurora. The shape of the Aurora active site binding pocket in the new crystal model is an equivalent shape to that of the first. The active site binding pocket of the original Aurora A crystal is defined by the amino acid residues of set A and their atomic coordinates as given in Tables 1 and 2. Equivalent shape is defined as having an rmsd of less than 1 Å upon superposition of the subset of least flexible amino acid residues (set B).

Thus, the invention provides a method to determine or design the three dimensional structure of a crystal form of Aurora by difference Fourier or Molecular Replacement, using the coordinates (Tables 1 and 2) of an Aurora A crystal to model the structure of a new Aurora crystal wherein the active site ATP binding region is equivalent to that in the first crystal. The method may be carried out as follows. An Aurora protein (wild type, mutant, variant or homologue) is purified and crystallised as a pure protein or in complex with an inhibitor compound. This crystal may have the same crystal form (same protein packing) as one of the crystal structures defined by Tables 1 and 2, or it may have a different crystal form (different protein packing). By taking diffraction measurements of the crystal and using the atomic coordinates in Tables 1 or 2 (or equivalent coordinates), it is possible to work out the structure of the crystal by the known methods of difference Fourier (same packing) or molecular replacement (different packing). This invention covers the use in drug design of the active site ATP binding pocket in any new crystal since this will be equivalent to that in the original crystal.

The invention further provides Aurora A proteins (including homologues, variants and mutants) designed by the above method. The Aurora A proteins may have identical properties to wild type Aurora A or may have one or more different properties compared to wild type Aurora A.

According to a further aspect of the invention, we provide a method to select or design chemical modulators (preferably inhibitors) of Aurora by using the Aurora A catalytic domain structure (including that of homologues, variants, mutants, and inhibitor complexes) and the shape of the active site ATP binding pocket (or an equivalent shape as previously defined). Information from the three dimensional atomic coordinates of the AMP-PNP molecule and its spatial orientation in relation to the three dimensional atomic coordinates of the Aurora A catalytic domain is used as a tool to design Aurora modulators (preferably inhibitors). In addition, information from the three dimensional atomic coordinates of the inhibitor molecule of formula II and its spatial orientation in relation to the three dimensional atomic coordinates of the Aurora A catalytic domain is used as tool to design Aurora modulators (preferably inhibitors). Small-molecule modulators of Aurora may be selected or designed to fit into the shape of the active site binding pocket.

Knowledge of the structural determinants that account for the difference in substrate specificity between Aurora A and other kinases, such as PKA, provides a foundation for the design of highly specific modulators of the Aurora A enzyme. Structural differences at the ATP binding pocket between Aurora and other kinases (defined by differences in the atomic coordinates of residues in the ATP pocket) may be used to design selective Aurora A modulators.

According to a further aspect of the invention, use of the coordinates of the Aurora A catalytic domain (Tables 1 and 2) to locate other pockets for interaction by small molecule modulators that affect Aurora activity is claimed. Such pockets may overlap with the active site ATP binding pocket or be completely independent. The three-dimensional structure of Aurora A kinase is an essential tool in the discovery of any such pockets that provide an alternative for modulator interaction to the active site ATP binding pocket.

As described above, the Aurora A crystal structure may be used in the rational design of drugs which modulate (preferably inhibit) the action of Aurora. These Aurora modulators may be used to prevent or treat the undesirable physical and pharmacological consequences of inappropriate Aurora activity.

The present invention will now be described with reference to the following non-limiting Examples.

Definition of Terms

In the Description (including the Examples) the following terms are used:

The term "atomic co-ordinates" refers to mathematical co-ordinates corresponding to the positions of every atom derived from mathematical equations related to the diffraction patterns obtained from a monochromatic beam of X-rays illuminating a crystal. The diffraction data are used to calculate an electron density map of the repeating unit of the crystal. The electron density maps are used to establish the positions of the individual atoms within the unit cell of the crystal. Those of skill in the art understand that a set of atomic co-ordinates determined by X-ray crystallography is not without standard error or experimental variation.

The term "unit cell" refers to the basic building block from which the entire volume of a crystal may be constructed.

The term "space group" refers to the arrangement of symmetry elements within a unit cell.

The term "molecular replacement" refers to a method that involves generating a preliminary model of a crystal whose atomic co-ordinates are not known, by orienting and positioning a related molecule whose atomic co-ordinates are known. Phases are then calculated from this model and combined with observed amplitudes to give an approximate Fourier synthesis of the structure whose co-ordinates are unknown.

Example 1: Production of the kinase catalytic domain of Aurora A

Molecular Biology:

In order to obtain a polypeptide (or protein) that can be utilised for determination of the three dimensional (tertiary) structure of Aurora A, DNA encoding Aurora A may be obtained by total gene synthesis or by cloning. This DNA may then be expressed in a suitable expression system to obtain a polypeptide that can be subjected to techniques to determine its three dimensional structure.

In this case, the human Aurora A gene carrying an artificially induced mutation (GAT to ACT in nucleotides 862-864, taking the A of the initial ATG in the open reading frame of the gene to be +1) encoding for a threonine to aspartate (T to D using the single letter amino

acid code) mutation of amino acid 287 (taking the first amino acid immediately after the initial methionine as amino acid number one) formed the basis of the expression construct used in these studies. This [T287D]Aurora A mutant was a gift of Dr. Jim Bischoff, SUGEN Inc. Since the full length [T287D]Aurora A protein expressed in *E.coli* was poorly soluble and aggregated on purification, a truncated mutant form was generated. The regions encoding for amino acids 94 to the stop codon of [T287D] Aurora A was amplified using the polymerase chain reaction (PCR). The 5' PCR primer (5'GATCGATCGGATCCACCCAAAAGAGCAAGCAGCCC 3'; SEQ ID NO.: 1) carried a spacer region (to allow efficient cleavage by restriction endonuclease), the BamH1restriction endonuclease recognition sequence and sequence corresponding to the bases 283-301. The 3' primer (5' TGACGCTAGGATCCCCTAAGACTGTTTGCTAGCTGATTC 3'; SEQ ID NO.: 2) carried a spacer region, BamH1 recognition sequence and 3' end of the Aurora A (bases 1189-1212) sequence including the stop codon. PCR products were purified and cloned in to the pCR-Script vector (Stratagene) using the pCR-Script AMP cloning kit (Stratagene. product # 211188) according to manufacturers directions. The pCR-Script vector carrying the [T287D] Aurora A (94-402) sequence was digested with BamH1, the digestion products resolved by agarose gel electrophoresis and the DNA fragment corresponding to the [T287D] Aurora A (94-402) sequence excised and purified using a Qiagen QIAquick kit (Qiagen product #28704). This fragment was then ligated into the vector pTB375NBSE, which had previously been cut with BamH1. (Details of the methods for the assembly of recombinant DNA molecules can be found in standard texts, for example Sambrook et al. 1989, Molecular Cloning – A Laboratory Manual, 2nd Edition, Cold Spring hbor Laboratory Press and Ausubel et al. 1999, Current Protocols in Molecular Biology, John Wiley and Sons Inc). The pTB375NBSE vector is derived from pAT153, which is a mobilization-minus derivative of pBR322. The inserted genes were under the control of a bacteriophage T7 promoter and therefore requires expression of the T7 polymerase in *trans* for efficient transcription in *E.coli*. The plasmid encodes tetracyline resistance for selection.

The ligation reactions were transfected in-to TOP10 competent *E.coli* (Invitrogen product #C4040-10) and *E.coli* carrying the pTB375NBSE recombinant vectors identified by their ability to grow on media containing tetracycline. Plasmid DNA was extracted from these bacteria and subjected to digestion with the restriction endonuclease EcoR1 to identify those carrying the [T287D] Aurora A (94-402) sequence. The identity of the insert was then confirmed by dideoxy chain termination DNA sequencing prior to protein expression.

pTB375NBSE carries the initiation codon (ATG) 3' to the T7 promoter and also the following sequence up to and including the BamH1 restriction endonuclease recognition site:

5'... ATG GGC CAT CAT CAT CAT CAC GGA TCC .....3' (SEQ ID NO.: 3)

Sequences inserted into the BamH1 site "in frame" with the initiation codon will therefore be expressed as a fusion protein with the following N-terminal fusion:

(N-terminal) MGHHHHHHGS.....(C-terminal) (SEQ ID NO.: 4)

The fusion of 6 histidines to proteins is commonly used to provide a "tag" for protein purification, usually by affinity for metal ions such as nickel. Since the [T287D] Aurora A sequence coding for amino acids 94-402 was inserted in to the BamH1 site, the plasmid encodes for the following protein (using the standard single letter amino acid code):

MGHHHHHHGSTQKSKQPLPSAPENNPEEELASKQKNEESKKRQWALEDFEIGRPLGK
GKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQLRREVEIQSHLRHPNILRLYGY
FHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITELANALSYCHSKRVIHRDIK
PENLLLGSAGELKIADFGWSVHAPSSRRTDLCGTLDYLPPEMIEGRMHDEKVDLWSL
GVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLISRLLKHNPSQRPML
REVLEHPWITANSSKPSNCQNKESASKQS. (SEQ ID NO.: 5)

This protein will be referred to in the text as MG-6His-GS-[T287D]Aurora A(94-402).

Based on the limited proteolysis studies (described later in Example 1), two additional truncated mutant forms of the Aurora A protein were also generated. The regions encoding for amino acids 113-400 and 122-400 of [T287D]Aurora A were amplified using the polymerase chain reaction (PCR). The 5' PCR primers (5'CATATGCTGGCATCAAAACAGAAAAATG 3' for 113-400 of [T287D]Aurora A or 5'CATATGTCAAAAAAGAGGCAGTGGGC 3' for 122-400 of [T287D]Aurora A) carried a Nde1 restriction endonuclease recognition sequence. A single 3' primer (5'GGATCCTCATTTGCTAGCTGATTCTTTGTTTTGG 3') was used for both constructs and carries a BamH1 recognition sequence and 3' end of the Aurora A sequence following the stop codon. PCR products were purified and cloned into the pCR-

Script vector (Stratagene) using the pCR-Script AMP cloning kit (Stratagene. product # 211188) according to manufacturers instructions and transfected into the *E. coli* strain DH5α (Invitrogen product #18258-012). The *E. coli* colonies containing the recombinant pPCR-Script [T287D]Aurora A(113-400) or pPCRscript [T287D]Aurora A(122-400) were identified by colony PCR screening using the primers T3 (5'AATTAACCCTCACTAAAGGG 3') and T7pro (5'TAATACGACTCACTATAGGG 3') hybridising specifically on either side of the pPCR script vector cloning site. The pPCR-Script vectors carrying the [T287D]Aurora A(113-400) or [T287D]Aurora A(122-400) sequence were prepared from *E. coli* and were digested with Nde 1 and Bam H1, the digestion products resolved by agarose gel electrophoresis. The fragments containing the [T287D]Aurora A(113-400) or [T287D]Aurora(122-400) were ligated into the expression vector pET28a (Novagen product #69864-3) between the Nde1 and BamH1 restriction sites. The inserted genes were cloned in frame with a sequence coding for a 6 histidine tag followed by a sequence encoding a thrombin protease cleavage site (see below for a complete description). The inserted genes are under the control of a bacteriophage T7 promoter and therefore require expression of the T7 polymerase in *trans* for efficient transcription in *E.coli*. The plasmid encodes kanamycin resistance for selection.

The ligation reactions were transfected into DH5α competent *E.coli* and the bacteria carrying the pET28a-[T287D]Aurora A(113-400) or pET28a-[T287D]Aurora A(122-400) recombinant vectors were identified by their ability to grow on media containing kanamycin. Plasmid DNAs were extracted from these bacteria and subjected to digestion with the restriction endonucleases Nde1 and BamH1 to identify those carrying the [T287D]Aurora A(113-400) or [T287D]Aurora A(122-400) sequences. The identity of the insert was then confirmed by dideoxy chain termination DNA sequencing prior to protein expression.

pET28a carries the initiation codon (ATG) 3' to the T7 promoter and also the following sequence up to and including the Nde1 restriction endonuclease recognition site:

5'... ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG .....3'

Sequences inserted into the Nde1 site "in frame" with the initiation codon will therefore be expressed as a fusion protein with the following N-terminal fusion (using the standard single letter amino acid code):

(N-terminal) MGSSHHHHHHSSGLVPRGSHM.....(C-terminal)

The fusion of 6 histidines to proteins is commonly used to provide a "tag" for protein purification, usually by affinity for metal ions such as nickel. The motif "LVPRGS" corresponds to a specific thrombin protease cleavage site that allows the proteolytic removal of the sequence "MGSSHHHHHHSSGLVPR" after incubation of the protein with thrombin. Since the [T287D]Aurora A sequences coding for amino acids 113-400 and 122-400 were inserted into the Nde 1 site, the plasmid encodes for the following protein (using the standard single letter amino acid code):

[T287D]Aurora A(113-400)
MGSSHHHHHHSSGLVPRGSHMLASKQKNEESKKRQWALEDFEIGRPLGKGKFGNVY
LAREKQSKFILALKVLFKAQLEKAGVEHQLRREVEIQSHLRHPNILRLYGYFHDATRV
YLILEYAPLGTVYRELQKLSKFDEQRTATYITELANALSYCHSKRVIHRDIKPENLLLG
SAGELKIADFGWSVHAPSSRRTDLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEF
LVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLISRLLKHNPSQRPMLREVLEHP
WITANSSKPSNCQNKESASK
This protein will be referred to in the text as MGSS-6His-SSGLVPRGSHM-[T287D]Aurora A(113-400)

[T287D]Aurora A(122-400)
MGSSHHHHHHSSGLVPRGSHMSKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFI
LALKVLFKAQLEKAGVEHQLRREVEIQSHLRHPNILRLYGYFHDATRVYLILEYAPLG
TVYRELQKLSKFDEQRTATYITELANALSYCHSKRVIHRDIKPENLLLGSAGELKIADF
GWSVHAPSSRRTDLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEFLVGKPPFEAN
TYQETYKRISRVEFTFPDFVTEGARDLISRLLKHNPSQRPMLREVLEHPWITANSSKPS
NCQNKESASK
This protein will be referred to in the text as MGSS-6His-SSGLVPRGSHM-[T287D]Aurora A(122-400)

Protein expression

pTB375NBSE carrying the [T287D] Aurora A (94-402) sequence were transfected into *E.coli* BL21(DE3) pLys S (genotype: B F⁻ *dcm ompT hsdS*(r_B^- m_B^-) *gal* λ(DE3) [pLysS Cam^r]). The strain was grown for 16 h (LB medium containing tetracycline (10μg/mL) and chloramphenicol (34μg/mL) at 30°C in shake flasks to OD_{550nm} ~5. This culture was inoculated into high biomass medium containing tetracycline (10μg/mL) and chloramphenicol (34μg/mL), in a 20 L fermenter (B. Braun, Melsungen, Germany). Cells were grown aerobically in fed batch culture at 30 °C, pH 6.7 with dissolved oxygen tension maintained at 50% air saturation. Expression of 6His-[T287D] Aurora A (94-402) was induced 12 hours post inoculation (OD_{550nm} ~13) with 0.40mM isopropyl-β-D-thiogalactopyranoside (IPTG), and cells harvested 3.0 hours later (OD_{550nm} ~33) by batch centrifugation (7,000xg at 4 °C for 30 min).

pET28a carrying the [T287D]Aurora A(122-400) sequence was transfected into *E.coli* DS410 (DE3) (a derivative of the original minicell-producing strain P678-54). The strain was grown for 30 h (M9 glucose medium containing kanamycin (25μg/mL) at 37°C in shake flasks to OD_{550nm} ~1.4. This culture was inoculated into high biomass medium containing kanamycin (25μg/mL) in a 20 L fermenter (B. Braun, Melsungen, Germany). Cells were grown aerobically in fed batch culture at 30°C, pH 6.7 with dissolved oxygen tension maintained at 50% air saturation. Expression of MGSS-6His-SSGLVPRGSHM-[T287D]Aurora A(122-400) was induced 16 hours post inoculation (OD_{550nm} ~19) with 0.10mM isopropyl-β-D-thiogalactopyranoside (IPTG), and cells harvested 23 hours later (OD_{550nm} ~26) by batch centrifugation (7,000xg at 4°C for 30 min).

Definition of kinase domain fragment

MG-6His-GS-[T287D]Aurora A(94-402) was purified from *E. coli* cell paste by Ni-NTA Agarose chromatography followed by size exclusion chromatography. The solution properties of this protein were found to be unfavourable for structural studies. Limited proteolysis of MG-6His-GS-[T287D]Aurora A(94-402) was used to identify fragments of the Aurora A kinase domain with superior solution properties. Aliquots of MG-6His-GS-[T287D]Aurora A(94-402) were subjected to proteolytic digestion with trypsin, thermolysin

or endoproteinase Glu-C (V8). Protein fragments were identified by analysis with Coomassie-stained SDS PAGE, electrospray mass spectrometry (ESMS) and N-terminal sequencing. Cleavage and purification was performed at sufficient scale to produce appropriate quantities of [T287D]Aurora A (122-396) for crystallisation, as detailed below. Characterization of these fragments of Aurora A was used to design additional constructs, including MGSS-6His-SSGLVPRGSHM-[T287D]Aurora-A(122-400). The molecular biology procedures used to generate MGSS-6His-SSGLVPRGSHM-[T287D]Aurora-A(122-400) are given in the Molecular Biology section of Example 1.

Lysis of E. coli containing MG-6His-GS-[T287D]Aurora A(94-402)

The following procedures were performed at 4°C unless otherwise stated. *E. coli* cell paste (200 g) was resuspended using a Kinematica PT6000 homogeniser (Kinematica GMBH, Basel, Switzerland) in 1.0 l of lysis buffer (40mM HEPES, 200mM NaCl, 2mM imidazole, 2mM 2-mercaptoethanol, 1mM benzamidine, pH 7.4). The cells were lysed using an Avestin EmulsiFlex ñC5 (Avestin, Inc., Ottawa, Canada), using a single pass at an average pressure of 10,000 psi. The resulting lysate was centrifuged at 17,000 x g (average) for 90 min before aspirating the supernatant and discarding the pellet.

Lysis of *E. coli* containing MG-6His-GS-[T287D]Aurora A(94-402)

The following procedures were performed at 4 °C unless otherwise stated. *E. coli* cell paste (200 g) was resuspended using a Kinematica PT6000 homogeniser (Kinematica GMBH, Basel, Switzerland) in 1.0 l of lysis buffer (40mM HEPES, 200mM NaCl, 2mM imidazole, 2mM 2-mercaptoethanol, 1mM benzamidine, pH 7.4). The cells were lysed using an Avestin EmulsiFlex ñC5 (Avestin, Inc., Ottawa, Canada), using a single pass at an average pressure of 10,000 psi. The resulting lysate was centrifuged at 17,000 x g (average) for 90 min before aspirating the supernatant and discarding the pellet.

Preparation of [T287D]Aurora A(122-396)

The following procedures were performed at 4°C unless otherwise stated.

A 26 mm diameter chromatography column packed with 25 mL Qiagen Ni NTA-Agarose (Qiagen GMBH, Hilden, Germany) was equilibrated with 10 column volumes of lysis buffer before loading lysate supernatant containing MG-6His-GS-[T287D]Aurora A(94-402) onto

the column at a flow rate of 0.9 mL/min. Using a flow rate of 2.0 mL/min the column was washed with 10 column volumes of wash buffer (40mM HEPES, 20mM imidazole, 2mM 2-mercaptoethanol, pH 7.5) to remove weakly bound or non-specifically bound impurities. Elution of bound protein was effected using elution buffer (40mM HEPES, 400mM imidazole, 2mM 2-mercaptoethanol, pH 7.5) at 2.0 mL/min. Eluted material was flowed through a second chromatography column (26 mm diameter, packed with 25 mL Pharmacia Q Sepharose Fast Flow (Amersham Pharmacia Biotech, Uppsala, Sweden) previously equilibrated with 10 column volumes of wash buffer). Fractions of 10.0 mL were collected, and after analysis by Coomassie-stained SDS PAGE, those fractions containing significant amounts of MG-6His-GS-[T287D]Aurora A(94-402) were pooled. At this stage the pool (approximately 200 mL) was stored in an airtight container at 4 °C for up to seven days.

From this stage forward, all procedures were carried out at room temperature, unless otherwise stated. A Pharmacia HiPrep 16/60 Sephacryl S-100 pre-packed size exclusion column was equilibrated in running buffer (40 mM HEPES pH7.5, 350 mM NaCl, 2 mM dithiothreitol (DTT)). The column was run at a flowrate of 1.0 mL/min. A 10 mL sample of the MG-6His-GS-[T287D]Aurora A(94-402) pool was centrifuged (31,000 x *g*, 4 °C, 60 min) and loaded onto the column. The fractions (2.0 mL) were analysed by Coomassie-stained SDS PAGE, and those containing MG-6His-GS-[T287D]Aurora A(94-402) were pooled.

Limited proteolysis at room temperature was carried out on the size exclusion chromatography-purified pool of MG-6His-GS-[T287D]Aurora A(94-402), whose concentration was 1 mg/mL. Using a mass ratio of 1 part protease to 100 parts MG-6His-GS-[T287D]Aurora A(94-402), endoproteinase Glu-C from *Staphylococcus aureus* V8 (Boehringer Mannheim UK, Lewes, Sussex, UK) was added to the pool. Proteolysis was allowed to continue for between 3 and 7 h.

A chromatography column was packed with a mixture of Pharmacia Sephacryl S-100 HR and Pharmacia Q-Sepharose high performance in the ratio of 9:1 v/v respectively (referred to as 'the S-100/Q column'). The column volume was 130 mL. It was equilibrated and run in S-100/Q running buffer (40 mM HEPES pH7.5, 50 mM NaCl, 2 mM dithiothreitol) at a flowrate of 1.0 mL/min. A sample of the proteolysed pool (8 mL) was loaded onto the S-100/Q column and 2.0 mL fractions were collected. Fractions were analysed by Coomassie-stained SDS PAGE, and those containing significant quantities of pure [T287D]Aurora A(122-396) were pooled. A sample of the pool was analysed by LC-ESMS using a Micromass

LCT in conjunction with a Waters Alliance HPLC (Micromass, Manchester, UK). A further sample of the pool was subjected to N-terminal sequencing. Once the identity of the cleaved protein had been confirmed as [T287D]Aurora A(122-396), it was submitted for crystallisation.

Preparation of GSHM-[T287D]Aurora A(122-400)

The following procedures were performed at 4°C unless otherwise stated.

A 26 mm diameter chromatography column packed with 15 mL Qiagen Ni NTA-Agarose (Qiagen GMBH, Hilden, Germany) was equilibrated with 10 column volumes of lysis buffer before loading lysate supernatant containing MGSS-6His-SSGLVPRGSHM-[T287D]Aurora-A(122-400) onto the column at a flow rate of 1.0 mL/min. Using a flow rate of 2.0 mL/min the column was washed with 7 column volumes of wash buffer (40mM HEPES, 200mM NaCl, 10mM $MgCl_2$, 20mM imidazole, 2mM 2-mercaptoethanol, pH 7.5) to remove weakly bound or non-specifically bound impurities. Elution of bound protein was effected using elution buffer (40mM HEPES, 400mM imidazole, 10mM $MgCl_2$, 2mM 2-mercaptoethanol, pH 7.5) at 2.0 mL/min. Fractions of 10.0 mL were collected, and after analysis by Coomassie-stained SDS PAGE, those fractions containing significant amounts of MGSS-6His-SSGLVPRGSHM-[T287D]Aurora-A(122-400) were pooled.

From this stage in the purification onward, all procedures were carried out at room temperature unless otherwise stated. A Pharmacia HiPrep 26/10 Fast Desalting pre-packed column was equilibrated in running buffer (40 mM HEPES pH7.4, 150 mM NaCl, 2 mM 2-mercaptoethanol). The column was run at a flowrate of 3.0 mL/min. A 10 mL sample of the MGSS-6His-SSGLVPRGSHM-[T287D]Aurora-A(122-400) pool was filtered (0.22μm) and loaded onto the column. Fractions were collected, and those containing the most concentrated amounts of MGSS-6His-SSGLVPRGSHM-[T287D]Aurora-A(122-400) were pooled.

Bovine thrombin (500 units, Amersham Pharmacia Biotech) was added to the pool of 50 mg (+/- 20%) of purified MGSS-6His-SSGLVPRGSHM-[T287D]Aurora-A(122-400) whose concentration was 1 mg/mL. Specific proteolytic cleavage was allowed to proceed to completion at 4°C, producing the truncated mutant GSHM-[T287D]Aurora A(122-400).

A Pharmacia HiPrep 16/60 Sephacryl S-100 pre-packed size exclusion column was equilibrated in running buffer (40 mM HEPES pH7.4, 50 mM NaCl, 1 mM dithiothreitol). The column was run at a flowrate of 1.0 mL/min. A 10 mL sample of the GSHM-

[T287D]Aurora A(122-400) pool was filtered (0.22μm) and loaded onto the column. Fractions (2.0 mL) were analysed by Coomassie-stained SDS PAGE, and those containing GSHM-[T287D]Aurora A(122-400) were pooled, and submitted for crystallisation.

Analysis

For SDS PAGE all samples were diluted in Laemmli buffer containing 2-mercaptoethanol, boiled for 2 minutes and loaded onto a 8-16% gradient, 1.5mm thickness x 10 well NOVEX gel (NOVEX, San Diego, California). Gels were stained with Coomassie blue R-250. Edman degradation was carried out on a Perkin Elmer 477A peptide sequencer (Applied Biosystems, Foster City, CA) with on-line detection of PTH amino acids. Mass spectra were acquired using a Micromass LCT with electrospray source (Micromass, Manchester, UK) and on-line Waters 2790 Alliance delivery system (Waters, Milford, MA). Protein was loaded directly on to a Phenomenex Jupiter 5μ C5 300_ 150 x 2.00 mm reverse phase column equilibrated in Milli Q water (Millipore, Bedford, MA), 2.7% acetonitrile, 0.1% trifluoroacetic acid, and the column was developed with a 2.7% to 90% acetonitrile gradient over 30 minutes at a flowrate of 80μl/min. A fraction (approximately 25%) of the eluted proteins passed into the mass spectrometer.

Example 2: Crystallisation of [T287D] Aurora A catalytic domain constructs

The [T287D] Aurora A(122-396):AMPPNP complex was crystallized at 15°C by the method of hanging-drop vapour diffusion. The protein [T287D] Aurora A (122-396) was concentrated to ~10 mg/mL solution (in 40mM HEPES pH 7.4, 2mM DTT, 50mM NaCl), 5mM AMP-PNP was then added to this solution and the complex was incubated on ice for 30 minutes. Prior to setting up crystallization trials this complex solution was microfuged for 10 minutes. The drops contained a 1:1 by volume mixture of complex solution and reservoir buffer (0.2M K_2HPO_4, 1.6M NaH_2PO_4, 0.1M phosphate/citrate buffer pH 3.8) giving a final 4μl drop volume. The [T287D] Aurora(122-396)-AMP-PNP crystals belong to space group $P3_221$ with unit cell dimensions $a = b = 86.55$ Å, $c = 78.34$ Å, and $\alpha=\beta=90°$, $\gamma=120°$, and contain 1 complex molecule per asymmetric unit. Before data collection, the crystals were transferred briefly (for about 20 seconds) to a cryobuffer containing 0.2M K_2HPO_4, 1.6M

NaH_2PO_4, 0.1M phosphate citrate pH 3.8, 30% glycerol before being cooled to 100K in a nitrogen gas stream.

The GSHM-[T287D] Aurora A(122-400) complex with the chemically synthesized inhibitor of formula II was crystallized as follows. Preparation of compound of formula II is described under example 19 in patent publication number WO 01/21597, publication date 29/3/01 (application number PCT/GB00/03593, international filing date 19/09/00). The compound was added at 5mM to a solution containing protein (GSHM-[T287D] Aurora A(122-400) at 10mg/ml, 40mM HEPES pH7.5, 50mM NaCl, and 1mM 2-mercaptoethanol. Drops were formed by mixing 1:1 volumes of protein complex solution and a reservoir solution containing 22% PEG 4000 and 0.2M ammonium sulphate. Crystallisation was achieved by hanging drop vapour diffusion at 15°C. Data were collected at room temperature from a crystal mounted in a capillary. The crystal could be translated in the X-ray beam to allow multiple exposures. The Aurora A-inhibitor crystals are of space group $P2_1$ with unit cell dimensions a = 52.6, b = 88.4, c = 67.8 Å, $\alpha = \gamma = 90$ and $\beta = 90.01°$, and contain two complex molecules in the asymmetric unit.

Example 3: Structure determination of [T287D] Aurora A catalytic constructs

Diffraction data were collected at beamline PX9.6 at the SRS, Daresbury on an ADSC Quantum 4 CCD detector. The data were indexed and integrated with the program Mosflm and scaled with the program SCALA (CCP4). Molecular replacement and rigid body refinement to a resolution of 3.0 Å were carried out using the program AMoRe. A search model was derived from mouse PKA, truncating the model at residues 32 to 310 and replacing all non-identical residues with Ala. 5% of the data were reserved at this stage as a cross-validation set and the initial model underwent torsion angle simulated annealing in the program CNX using a maximum likelihood target and an overall anisotropic temperature factor correction. The model then underwent iterative rounds of manual rebuilding and simulated annealing until the working R-factor fell below 30%, at which point restrained isotropic individual temperature factor refinement was carried out. Concurrent building of both inhibitor complexes with the same Aurora protein in different crystal forms proved very instructive when it came to clarification of regions that were difficult to interpret. Further iterative rebuilding and addition of waters was carried out until the free R factor converged.

Crystallographic data and refinement statistics are given in tables 4 and 5.

Table 4: Aurora-AMPPNP complex data and refinement statistics.

Space Group	$P3_221$
Cell constants	a=b=86.55, c= 78.34Å α=β=90, γ=120°
Reflections	62278
Independent Reflections	17003
R_{sym} (2.25-2.2 Å)	3.6% (32.6%)
Resolution (Å)	38-2.2
I/sigI (2.25-2.2 Å)	19.3 (3.0)
Completeness (2.25-2.2 Å)	97.1% (83.2%)
$R_{(free)}$, $R_{(work)}$	23%, 28%
Rmsd (bond lengths)	0.006
Rmsd (bond angles)	1.2

Table 5 : Aurora-inhibitor complex data and refinement statistics:

Space Group	$P2_1$
Cell constants	a=52.6, b=88.4, c=67.8Å α=γ=90, β=90.01°
Reflections	36664
Independent Reflections	26294
R_{sym} (2.25-2.1 Å)	6.6% (30.5%)
Resolution (Å)	52-2.1
I/sigI (2.25-2.1 Å)	7 (2.1)
Completeness (2.25-2.1 Å)	72.5% (25.5%)
$R_{(free)}$, $R_{(work)}$	22%, 27%
Rmsd (bond lengths)	0.019
Rmsd (bond angles)	1.8

Example 4: Description of the Structure of Aurora A kinase

The structure of [T287D] Aurora A (122-396) in a binary complex with the ATP analogue AMP-PNP has been solved to a resolution of 2.2 Å. The structure of GSHM-[T287D] Aurora A(122-400) in a binary complex with the synthetic inhibitor of formula II has been solved to a resolution of 2.1 Å. The structures contain the residues of the kinase catalytic domain. The kinase domain of [T287D] Aurora A shows the bilobal structure characteristic of protein kinases with the ATP and inhibitor binding site situated between the two lobes. The N-terminal domain (lobe) comprises a twisted β-sheet and a single kinked helix. The C-terminal lobe comprises mainly helices but also includes a small region of β-sheet. Parts of the polypeptide chain are disordered. In particular, the activation loop, residues 279 to 290 containing the T287D substitution, is not visible in the electron density. The disordered nature of the activation loop is a common feature in kinase crystal structures.

The structure adopts a conformation typical of catalytically inactive kinases, despite the introduction of the constitutively active mutation, T287D. It is thought that the acidic pH at which the crystallisation experiments were carried out will result in the introduced aspartate being protonated, and thus no longer able to mimic the phosphorylated threonine in the wild-type activated protein. The kinase activity of the mutant enzyme towards a peptide substrate was measured at varying pH values, as shown in Figure 3, and indeed, activity is significantly reduced falls as the pH is lowered.

The inactive conformation seen in our [T287D] Aurora A complexes is clearly capable of binding the inhibitor of formula II and the ATP analogue, and therefore allows structure-based design, which needs to make allowances for the flexibility and conformational changes that the kinase may undergo, for example, between its active and inactive states. In the case of the inhibitor, the inactive conformation may be forced by the steric bulk of the inhibitor.

Aurora A is quite closely related to the cyclic AMP-dependent protein kinase, also known as PKA, and the structures superpose with an overall rmsd of 1.4Å. The ATP binding cleft of Aurora A is more extended than the equivalent cleft in PKA on account of a shift in the position of a helix, formed by residues 174 to 182 in the N-terminal lobe. In the structure of [T287D] Aurora A, the helix is displaced approximately 3Å away from the ATP binding pocket compared with the equivalent helix in PKA, thus extending the length of the cleft

between the two lobes. The extended cleft can be exploited by elongated inhibitor molecules such as that of formula II and may be key to the design of specific inhibitors. The conserved DFG motif (Asp273Phe274Glu275) preceding the activation loop is apparent in the electron density. This region contains an aspartate residue necessary for catalysis. The glycine-rich loop, which is important for ATP binding in all kinases, shows good electron density throughout the main chain atoms, although the temperature factors are quite high, indicating significant mobility of the loop. However, the density for the side chains of some residues, such as Phe 143, is poor, and these are likely to adopt multiple conformations.

The AMP-PNP molecule adopts a dual conformation (Fig. 1). The adenine ring and ribose moiety in both conformations occupy similar locations with respect to the kinase molecule. Classical hydrogen-bonding interactions are made between the adenine ring and the hinge region of Aurora A. These are between N6 of the adenine ring and the main chain oxygen of Glu 210 and between N1 of the adenine ring and the main chain nitrogen of Ala 212. The differences in the two conformations arise from torsion angle differences between the ribose ring and the phosphate groups and also in torsion angles of phosphorus-oxygen bonds. In one conformation, the β-phosphate group forms a hydrogen bond to a water molecule, which, in turn, forms a hydrogen bond to Asp 273. In the other conformation, the β-phosphate forms hydrogen bonds with Ser 277 and Gln 260. In both conformations the α-phosphate forms a salt-bridge with Lys 161, and also forms a hydrogen bond with the main chain nitrogen of Val 278. No electron density for the γ-phosphate is present in either conformation suggesting a high degree of disorder. This disorder of the γ-phosphate has also been seen in other crystal structures, for example that of Checkpoint kinase.

The molecule of formula II also binds in the ATP binding site in the cleft between the two domains in the Aurora A kinase molecule. The molecule of formula II adopts an extended conformation, which demonstrates the extent of the available binding pocket (Fig 2b). A classical kinase (adenine-mimetic) inhibitor hydrogen bond interaction with the main chain peptides is made between N(17) in the inhibitor and the amide of amino acid residue 212. The piperidine moiety of the inhibitor extends into solvent (on the left in Fig 2b). At the other extreme of the inhibitor (right end in Fig 2b) the benzoyl moiety fits into a hydrophobic pocket formed by residues Leu163, Leu181, Leu195, Leu207 and Trp276. This inhibitor represents a more interesting start point for design than AMPPNP since protein regions more remote from the ATP location are explored, and this may help achieve specificity.

CLAIMS

What we claim is:

1. A crystalline form of a polypeptide comprising the catalytic domain of Aurora kinase.

2. A crystalline form according to Claim 1, wherein the polypeptide is an Aurora A kinase.

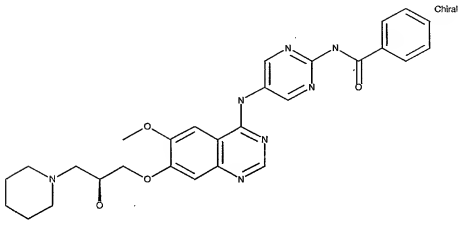
3. A crystalline form according to Claim 1 or Claim 2, wherein the crystalline form has the space group $P3_221$ or the space group P2.

4. A crystalline form according to any one of the preceding claims, wherein the crystalline form has unit cell dimensions a=b=86.55, c= 78.34 Å, α=β=90 and γ=120° or unit cell dimensions a = 52.6, b = 88.4, c = 67.8 Å, α= γ = 90 and β= 90.01 °.

5. A crystalline form according to any one of the preceding claims, wherein the catalytic domain comprises a binding site, wherein the binding site is defined by the x,y,z-coordinates of atoms in the set of amino acid residues given by the list: Arg136, Leu138, G1y139, Lys140, Gly141, Va1146, Ala159, Lys161, Leu163, Va1177, Glu180, Val181, Ile183, G1n184, Leu193, Leu195, Leu207, Leu209, G1u210, Tyr211, Ala212, Pro213, Leu214, G1y215, Thr216, Arg219, G1u259, Asn260, Leu262, A1a272, Asp273, Phe274, G1y275, Trp276, Ser277, Va1278, and His279 or their equivalent, wherein the atomic coordinates are listed in Tables 1 and 2; or wherein the binding site is defined by the x,y,z-co-ordinates of atoms in the set of amino acid residues given by the list: Arg136, Leu138, Gly139, Va1146, Ala159, Lys161, Leu163, Ile183, G1n184, Leu193, Leu195, Leu207, Leu209, Glu210, Tyr211, A1a212, Pro213, Leu214, G1y215, Thr216, Arg219, Glu259, Asn260 and Leu262 or their equivalent, and wherein the x,y,z-coordinates are within a root mean square deviation of not more than 1.0 Å of the coordinates listed in Tables 1 and 2.

6. A crystalline form according to any one of the preceding claims, additionally comprising an Aurora kinase inhibitor in complex with the catalytic domain of Aurora kinase.

7. A crystalline form according to Claim 6, wherein the Aurora kinase inhibitor is a compound of formula II:



Formula II.

8. A method of designing an Aurora chemical modulator using the atomic coordinates of a crystalline form according to any one of claims 1 to 5.

9. A method of selecting an Aurora chemical modulator using the atomic coordinates of a crystalline form according to any one of claims 1 to 5.

10. A method of designing an Aurora protein using the atomic coordinates of a crystalline form according to any one of claims 1 to 5.

11. A method of designing or selecting an Aurora modulator comprising the steps of: (a) exploring the atomic coordinates of Aurora as presented in Table 1 and Table 2 for information on the three-dimensional characteristics of the protein surface; (b) arriving at an alternative overlapping or non-overlapping binding pocket to the active site ATP binding pocket; and (c) selecting or designing an Aurora modulator using the binding pocket information.

12. A method of designing the three-dimensional structure of a second crystal form of Aurora kinase comprising the step of applying difference Fourier or molecular replacement methods using the atomic coordinates of an original crystal as presented in Table 1 and Table 2 to model the structure of the crystal second form, wherein the active site ATP binding pocket of the second crystal form is equivalent to that in the original crystal.

13. A method of designing or selecting an Aurora kinase modulator using the coordinates of any protein shown by this invention to possess structural similarity or relevance to Aurora kinase.

14. A method for designing a homologue of Aurora kinase that mimics the three-dimensional structure of Aurora kinase, which comprises:

(i) determining the three-dimensional coordinates of atoms of an Aurora kinase;

(ii) providing a computer having a memory means, a data input means, a visual display means, said memory means containing three-dimensional molecular simulation software operable to retrieve co-ordinate data from said memory means and to display a three-dimensional representation of a molecule on said visual display means and being operable to produce a modified three-dimensional homologue representation responsive to operator-selected changes to the structure of the Aurora kinase and to display the three-dimensional representation of the modified three-dimensional homologue;

(iii) inputting three-dimensional co-ordinate data of atoms of Aurora kinase into the computer and storing said data in the memory means;

(iv) inputting into the data input means of said computer at least one operator-selected change in structure of the Aurora kinase;

(v) executing said molecular simulation software to produce a modified three-dimensional molecular representation of the homologue structure;

(vi) displaying the three-dimensional representation of the homologue on said visual display means, whereby changes in three-dimensional structure of the Aurora kinase resulting from changes on structure can be visually monitored;

(vii) repeating steps (iv) through (vi) to produce a multiplicity of homologues;

(ix) selecting a homologue structure represented by a three-dimensional representation wherein the three-dimensional configuration and spatial arrangements of the kinase catalytic domain remain substantially preserved, thereby producing a homologue of Aurora kinase that mimics the three-dimensional structure of the Aurora kinase.

15. A method of producing a modulator of Aurora kinase comprising identifying a compound or molecule or designing a compound or molecule that fits into the active site ATP

binding pocket of the Aurora kinase, wherein the ATP binding pocket is defined by the x,y,z-coordinates of atoms in the set of amino acid residues given by the list (a) Arg136, Leu138, Gly139, Lys140, Gly141, Val146, Lys161, Leu163, Val177, Glu180, Val181, Ile183, Gln184, Leu193, Leu195, Leu207, Leu209, Glu210, Tyr211, Ala212, Pro213, Leu214, Gly215, Thr216, Arg219, Glu259, Asn260, Leu262, Ala272, Asp273, Phe274, Gly275, Trp276, Ser277, Val278, and His279, the atomic coordinates being listed in Tables 1 and 2 or (b) the x,y,z- coordinates of atoms in the set of amino acid residues given by the list Arg136, Leu138, Gly139, Val146, Ala159, Lys161, Leu163, Ile183, Gln184, Leu193, Leu195, Leu207, Leu209, Glu210, Tyr211, Ala212, Pro213, Leu214, Gly215, Thr216, Arg219, Glu259, Asn260 and Leu262, each having coordinates as described in Tables 1 and 2, thereby producing a modulator of Aurora kinase.

16. A crystalline form wherein the catalytic domain comprises a binding site , wherein the binding site is defined by the x,y,z-co-ordinates of atoms in the set of amino acid residues given by the list: Leu138, Gly139, Val146, Lys161, Val177, Arg178, Arg179, Glu180, Val181, Glu182, Ile183, Gln184, Leu193, Leu209, Tyr211, Ala212, Gly215, Thr216, Glu259, Asn260, Leu262, Ala272, Asp273, Phe274, Gly275, Trp276, Ser277, Val278 and His279 or their equivalent, wherein the atomic co-ordinates are listed in Table 1a.

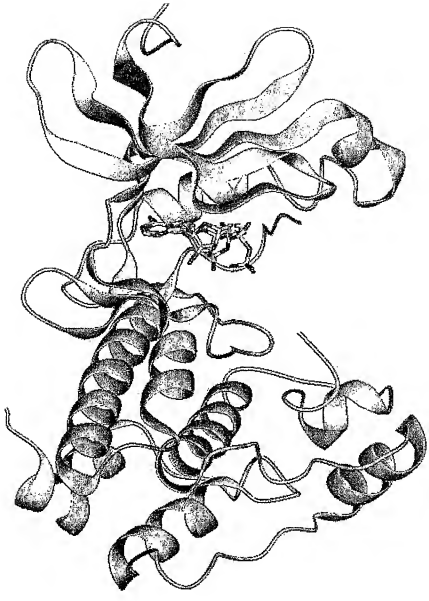


Figure 1

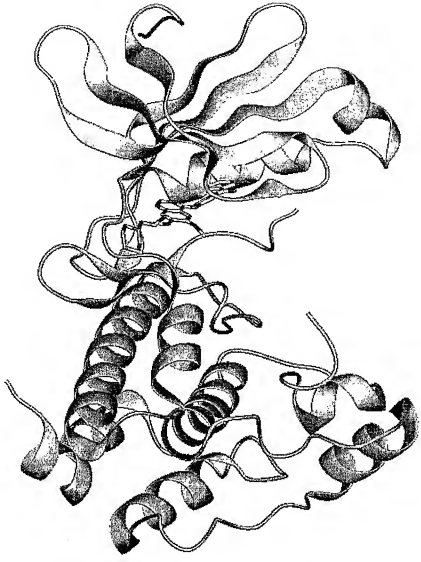


Figure 2a

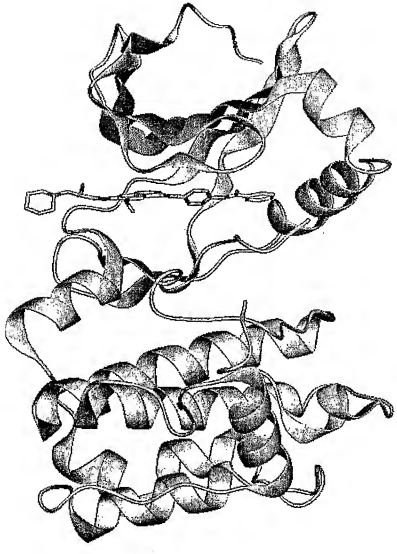


Figure 2b

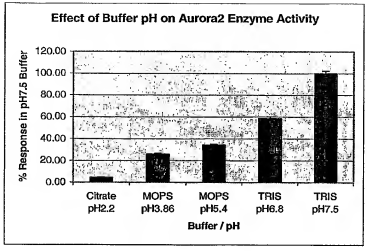

Effect of Buffer pH on Aurora2 Enzyme Activity
% Response in pH7.5 Buffer
120.00
100.00
80.00
60.00
40.00
20.00
0.00
Citrate pH2.2
MOPS pH3.86
MOPS pH5.4
TRIS pH6.8
TRIS pH7.5
Buffer / pH

Figure 3